A STUDY OF SPONTANEOUS MUTATION

BY

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UNIVERSITY OF CALIFORNIA PRESS
BERKELEY AND LOS ANGELES
1945

UNIVERSITY OF CALIFORNIA PUBLICATIONS IN ZOÖLOGY
EDITORS (BERKELEY): S. F. LIGHT, E. R. HALL, HAROLD KIRBY, A. H. MILLER

Volume 49, No. 10, pp. 291–550, plates 23–30, 4 figures in text, 153 tables

Submitted by editors May 12, 1944
Issued February 20, 1945
Price, $3.00

UNIVERSITY OF CALIFORNIA PRESS
BERKELEY AND LOS ANGELES
CALIFORNIA

CAMBRIDGE UNIVERSITY PRESS
LONDON, ENGLAND

PRINTED IN THE UNITED STATES OF AMERICA

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I. INTRODUCTION

In 1935 an interesting spontaneous outbreak of "mutation" was discovered which seemed to belong to the group of mass mutation. A few preliminary notes have been published on the findings; but although they give a correct general description of the facts, they also include errors in the analysis of results based on incomplete data. Personal circumstances have twice enforced long interruptions of the thorough analysis since begun, and consequent repetitions of the experiments. Publication of the facts *in extenso* now seems justified, since the happenings appear to be of basic importance for an understanding of the phenomenon of mutation.

Though natural, spontaneous mutation is the most important phenomenon of genetics, upon which the whole structure of classic genetics is built, our knowledge of it is nevertheless meager since hardly any systematic effort has been made to understand it (see, however, Baur, 1918). Mutants are usually picked up in the field, the pen, the bottle. Sometimes they are derived from pedigreed broods, and it is known how many gametes have mutated and at which point in the germ-cell cycle. But this is about the limit of information available, though certain features ought to have diverted research toward more detailed observations. Looking over the old literature on *Drosophila*, one finds, for example, such data on the origin of standard mutants as the following: Truncate was obtained in Beaded stock; both balloon and vestigial from truncate; purple from vestigial; kidney from vestigial and purple (N.B.: kidney frequently reappears in pure inbred vestigial cultures!); ebony from balloon; rough from truncate; spread from Beaded and vestigial; cardinal from vestigial × wild; plexus from spread. Here eleven standard mutations have a common pedigree. Other examples are: bow from rudimentary × wild; Bar from the same, as also blistered and jaunty; curved also was obtained from rudimentary. A great many standard mutants appeared in crosses of other mutants: Sepia from Lobe × dachs; Dichaete from cleft × sable forked; bithorax from maroon × wild; ski from white × wild; hairless from pink spineless × telescope; divergent from Star × telegraph; hairy from singed × inflated forked Bar; black from miniature × wild; gap from black × arc; dachs from sable × wild; comma from dachs × pink; morula from peach × wild; fringed from jaunty × white; etc.

All this may be a matter of chance, based upon the unintentional selection of experimental procedure and completely insignificant. It may, for example, be owing to the fact that mutant stocks and crosses were watched more carefully. But it is equally possible that a rule is hidden behind these facts and that a systematic study of spontaneous mutation will show that mutation is not haphazard.

A small but significant group of facts (aside from the important facts of radiation genetics) is available to show that mutation may occur occasionally as a mass phenomenon. The cases thus far made known (Demerec, Plough-Holthausen, Spencer, Valadares, Goldschmidt) have been discussed by me previously (Goldschmidt, 1940). Since that time new cases that have been more closely followed than the earlier ones have been reported by Neel, and by Tiniakoff; and Demerec

has recently announced (1943) that he has found yet another case. Thus far none of these have been analyzed in such a way as to make it possible to state with certainty what had actually happened. Since more details are known in the case to be described in this paper, it seemed advisable to put the data on record and to show that mutation might be something which is concerned not merely with the locus in question. In the course of this work numerous side lines connected with it had to be taken up. Some of them have been included here, though they might have been published separately, because I thought there should be on record at least one case in which the material used had been thoroughly tested. They might not seem very important if viewed on their own merits; yet as part of the whole they should, I thought, be included. In spite of much work not everything could be cleared up completely. It will be easy to suggest further experiments which should have been made at one point or another. But any piece of work involving innumerable details must one day be regarded as finished for the time being; and though I am conscious of the gaps still existing in the present work, I thought that this moment had now come.

ACKNOWLEDGMENTS

In the course of the years since 1935 I have been favored with much assistance. During 1936–1937, while my work was being transferred from Berlin to Berkeley, where all laboratory facilities had to be created afresh, Professor Curt Stern, of the University of Rochester, kept my stocks of *Drosophila* and returned them to me intact. I am deeply grateful for this kindness. The Department of Zoölogy of the University of California and its entire staff did everything possible, in an overcrowded building and within the means allowed by a not too plentiful budget, to make room and supply equipment for myself and for the research group which was to be built up. I am under great obligation to my colleagues who made this possible even at the cost of personal sacrifices. The Committee on Research of the University has allocated to me, year by year, funds for research assistants, and has repeatedly granted extra funds for special needs. I beg to express my gratitude to this Committee and to President Robert Gordon Sproul and Vice-President Monroe E. Deutsch, to whom I never appealed in vain. While the WPA organization was in existence, my work and that of my group of collaborators was accepted as a WPA project, and all the technical help needed was furnished freely—assistance for which I shall always be grateful to this organization and to its Supervisor for the Biological Sciences, Dr. R. Stohler.

The junior authors of the present paper have all served at some time during these years as research assistants[1] and have shared in the experiments, especially in repeating on a larger scale the findings of the senior author. He alone assumes the responsibility for the work, especially the decisive experiments, and for the presentation of the results. Mr. Masuo Kodani and Miss Aloha Hannah did all the cytological work. No result was accepted which could not be seen identically by both the senior author and the assistant, the former alone taking the responsibility for the data. Mrs. Richard M. Eakin kindly contributed the statistical work, of which only a part is incorporated in this paper. We are much obliged to Mrs. Laura G. Rauch for editing the manuscript.

[1] Richard Blanc is now at the University of Rochester; Ruth Fields, at the University of British Columbia; Claude Villee, at the University of North Carolina; and Werner Braun is now with the Division of Veterinary Science, Department of Agriculture, of the University of California.

II. THE STARTING POINT

A stock bottle of plexus flies started from the original Columbia stock seven years before and never appearing to be different from the standard type was found to contain (winter, 1933–1934) a majority of flies very different from the typical plexus as found in the other bottles. The venation showed an extreme type of plexus formation far beyond that of the mutant plexus (details will be given further on). Also, about half the females and a few rare males were blistered. In the great majority of individuals this blister (filled with fluid in the young flies and covering a considerable part of the wing, which is frequently torn when the blister breaks) is found on one wing only. I was originally interested in this problem of asymmetry and began inbreeding and selecting this stock in many different ways. An account of some of this work will be presented below. (Among the Pasadena stocks a line exists, listed in *DIS* as px bs seh, which is phenotypically very similar to the stock described. A note from the Pasadena stock keeper says that it is probably an allele of bs blistered. We shall see that the bs-locus is also involved in our line.) The line, which will be called plexus blistered in a purely descriptive sense, was controlled through many generations of brother-sister matings and remained constant. It has now been bred for about ten years. It has remained constant except for the features to be described, but in later years some of the characteristics of blistering became variable (details below). In a series of brother-sister matings in 1934–1935, 134 matings gave 10,795 ♀, 10,199 ♂. Among these were found, besides a number of individuals with half thorax or with abnormal abdomen—conditions which did not seem to be inherited—the following atypical individuals:

9 ♂ one wing like rudimentary or dumpy	1 ♂ dwarf
2 ♀, 2 ♂ spread wings	1 ♂ beaded
1 ♀, 2 ♂ shortened broad wings	

It will be noted later that these types, which did not seem to be inherited in simple tests, are all represented among the genuine mutations derived from this stock. They appeared in these lines after the manner of mutants, but were not isolated at that time because the work was originally not concerned with mutation. In the stock bottles no such types have been found.

On December 8, 1934, a pair from a closely inbred plexus blistered stock (abbreviated px bl, which does not signify any locus) was mated, a female with blisters on both wings and a male without blisters. The offspring were (besides the extreme plexus always present and therefore not mentioned):

No. 4100 B[1] 53 ♀ 46 ♀ one wing blistered, 2 ♀ both wings blistered
103 ♂ 2 ♂ blistered

A second generation was bred from both females with both wings blistered and the two blistered males (nos. 4302 and 4303):

No 4302 B 77 ♀ 40 ♀ blistered, 2 ♀ both wings blistered
72 ♂ 2 ♂ blistered

This resembles the foregoing generation except for the small number of males. (See later discussion of sex ratio in px bl.)

No. 4203 B 5 ♀ px blistered, 4 ♂ px 1 ♂ hemithorax

[1] B signifies work done in Berlin, 1934–1936. Record numbers of later work begin again with no. 1.

There had frequently been sterile pairs, but never a semisterility of this type. (The parents left in the bottle were still alive at the time of hatching.) Furthermore, never had all females been blistered. Otherwise these individuals were typical plexus blistered. From these a third generation was bred. One fertile pair (the only available virgin ♀) gave:

No. 4474 B 136 ♀ and 70 ♂ wild type (no plexus or blistered)
18 ♀ and 19 ♂ low-grade plexus like the typical mutant plexus
1 ♂ rudimentary

Again the parents were still in the bottle when the first count was made. These numbers are perfectly regular. They suggest that about 7/8 of the females and about 3/4 of the males were normal; 1/2 of the wild-type males were missing, 1/8 of the females and of the potential males (if the sex ratio were normal) being typical plexus, and a single individual was rudimentary (turning out to be an allele of r). This regularity, together with the presence of the parents and the further behavior of the line, excludes any error. No contamination is imaginable which would give this result. (See below.) It suggests that something involving an autosome and the sex chromosome (ratio 7:1, 1/2 of the males lethal) had occurred, which resulted in the disappearance of whatever it was that caused the extreme plexus and the blistered type in one combination, and the disappearance of the plexus type, at least phenotypically, in the rest. The rudimentary male might be an ordinary mutant at this locus, as such a mutation is said to be rather frequent, though it never occurred in my stocks (for a single recurrence see below). The following facts will show that this is not the case. *I wish to emphasize again the fact that all the offspring of the plexus blistered pair derived from a long constant pedigree were different from the parents.*

The rudimentary male cauld not be mated successfully. A fourth generation was bred from wild-type as well as from plexus flies, with the result recorded in table 1. The data show that some of the wild-type females and males were true-breeding (later extracted). Some females were heterozygous for rudimentary, producing less than 1/2 rudimentary males (rudimentary is less viable.) Another wild-type female was heterozygous for rudimentary in one X chromosome and for a new type with pointed wings in the other, which turned out to be a new allele of silver. Some of the females of this brood 4612 showed an indication of pointed wings (slight dominance effect). The combination of two plexus flies produced a typical plexus blistered brood with a relatively small proportion of blistered females, but with reappearance of the strong plexus type of venation lost in the foregoing generation. The changes, then, had begun with a "return mutation" to plus^{px} in the gametes of px bl, an event which somehow simultaneously released pointed and rudimentary. It may be anticipated that px bl contains also a mutant condition at the bs locus. This also had disappeared, and a male lethal had appeared.

It is to be emphasized that neither the rudimentary nor the pointed wing, which is also a pure-breeding sex-linked type (actually a silver allele), could have arisen by ordinary mutation. As some of the wild-type females were heterozygous for one or both, a mutation ought to have occurred in the sperm of the grandfather, who could have sired neither a rudimentary son nor a daughter heterozygous for both pointed and rudimentary in different X chromosomes (except by double mutation

and male crossing over). Also, three out of four wild-type daughters would have had to be sired by sperms with the rudimentary mutation. Furthermore, there is the nonconforming rudimentary male (among 90) in F_3.

The details of the following generations belong to the special analysis of the types produced and will be found in the respective sections further on. It turned out that the wild-type individuals could be either pure-breeding or heterozygous for rudimentary, pointed, or typical low-grade plexus in different combinations. (The bs allele was absent.) The decisive point is that a true-breeding wild type was established that was not distinguishable from any other. The pointed wing was easily isolated as a sex-linked recessive located at the left of the X chromosome. It is an allele of silver and it has bred true for years. The rudimentary type also was isolated. It was homozygous, heterozygous, or neither, for something producing plexus, and it could also contain pointed. It behaved as an allele to standard rudimentary and showed the same peculiarities (like female sterility). In stocks over double yellow it bred true, but frequently changed the phenotype (independently of external conditions) between medium-sized, dumpy-shaped wings and very short ones and other types (see below). The viability decreased with shortness, and the extremes produced only female offspring by inviability of the males, all transitions existing. The plexus blistered type recovered from the lines described above bred true to this type and was obviously again the old plexus blistered stock, thus showing that everything had happened within this stock. The type with a moderate amount of plexus was again heterozygous for pointed or rudimentary or both. Or it bred true, and has remained so for years, never producing a blistered or high-grade px fly. It behaves in tests with standard plexus as if it were identical with it. We point to the one dwarf (not producing offspring) in F_4, as dwarf reappeared again.

TABLE 1

OFFSPRING OF 4474

No.	Parents 4474[2]	+		Pointed ♂	Highgrade px of original type		px blistered ♀	Rudimentary ♂	
		♀	♂		♀	♂			
4609 B	+ × +	148	170	..	..	..	..	..	
4610 B	+ × +	185	80	..	..	..	..	37	
4612 B	+ × +	151	..	65	..	..	..	55	
4613 B	+ × +	8	3	..	..	..	..	1	1 dwarf
4614 B	px × px	...	..	..	72	67	13	..	

In one of the lines derived from the original abnormal brood other genetic types appeared. From the brood 4612 (see table 1), which had yielded normal females and pointed and rudimentary males, a further generation was bred from a normal female with a rudimentary male (no. 4764 B). It produced:

76 ♀ +	25 ♀, 15 ♂ low-grade plexus, not pointed
33 ♂ pointed	29 ♀, 32 ♂ rudimentary

The mother, then, was heterozygous for rudimentary; but only ¼ of the daughters, though nearly ½ of the sons, were rudimentary. The other X of the mother must

have contained pointed, and accordingly ½ of the males are pointed. Furthermore, both parents must have been heterozygous for plexus, which, however, did not show the recombination with pointed (it was not checked for rudimentary)—but this has no special meaning, as only some alleles of pointed can be clearly distinguished in the presence of plexus, which tends to make the wing tip appear blunted. Also, about half of the expected males were missing. A pair of plexus flies from the foregoing brood was mated (no. 4988 B), with the result:

62 ♀, 35 ♂ plexus like mother	.. 24 ♂ rudimentary
9 ♀, 7 ♂ plexus and pointed	1 ♀, 3 ♂ plexus, soft spread blistered

Here, first a plexus and pointed phenotype occurs in a ratio among the plexus flies which looks like 7:1, and the mother was heterozygous for rudimentary, as expected, though the number of r ♂ is deficient. A new type appears in a few individuals, exhibiting the same plexus as the parents and soft spread blistered wings. (Again we anticipate the genetic constitution of these flies. A full discussion of the entire story with additional facts will be given in a later section. These flies are homozygous for px and for a pointed allele, called $svr^{poi\ bl}$. Furthermore, they are homozygous for a second chromosome recessive at the arc locus, to be described as broad angular (bran). The combination bran and standard pointed produces what will be described later as soft blistered flies. The soft spread blistered type, however, is the result of recombination of bran with a new allele of poi, poi blist ($svr^{poi\ bl}$), which thus arose simultaneously with bran (see full discussion later). The px pointed phenotype turned out to be heterozygous bran with the new pointed allele.

These, then, were the original happenings anticipating part of the interpretation which will be presented further on. To enumerate the main features:

1) A standard plexus stock had changed in the stock bottle into the px bl type, which turned out to be mainly a combination of px, different bs alleles, a sex-linked locus connected with blistering, and autosomal modifiers for the degree of plexation.

2) In a large set of pair breedings from px bl for purposes of selection the entire offspring of a single pair was spontaneously different from the parents. In ordinary genetic language, the happenings would have to be described in the following way:

a) The original homozygous low-grade plexus which had disappeared as such in the formation of the high-grade plexus blistered stock from px had reappeared as true-breeding plexus (without bs).

b) This plexus mutant locus, as well as bs, had completely reverted in other flies, producing a true-breeding wild type.

c) The parental plexus blistered type which was absent in F_1 was recovered in F_2 and again bred true.

d) A new type with pointed wings was produced which turned out to be an allele of silver (svr^{poi}).

e) A new type of rudimentary was produced, indistinguishable from the standard mutant of this name and combined or not with plexus blistered and svr^{poi}.

f) A weak type with soft spread blistered and plexus wings segregated later, which turned out to be a recombination of px, another svr allele $svr^{poi\ bl}$, and an arc allele named bran.

g) Sex-linked lethals and strange ratios were present.

When these facts were first determined we tried to check on the possibility of an

experimental error, as the change of all the progeny from the type of the parents is an event to be looked upon with suspicion. It has already been mentioned that the parents were still in the bottle when the offspring started hatching. But let us suppose that this does not exclude contamination. From the results obtained, such contamination would have had to be with a wild-type fly. Further, one must suppose that pointed, rudimentary, pointed blistered, and bran were already present in the px bl stock but remained invisible until freed from px by a cross. What we considered to be the offspring of px bl flies would then have to be at least grandchildren of the supposed contamination, with the first contaminated generation looking like px bl. It would also have to be assumed that two alleles of silver and bran were hidden in the grandparents without showing their well-known effects, in addition to rudimentary in a male X without showing it, etc. This is more than the worst pessimist could expect.

Actually, genetical analysis of the px bl stock, which was started at once, never betrayed the presence of svr^{poi} or bran or rudimentary in the stock. But the decisive point is that all these mutants were later obtained many times from px bl as well as from other pedigreed derivatives of this stock, which obviously is likely to produce these mutants (and also others) under certain conditions. It is to be regretted that a complete repetition of all the features just described in the offspring of a single pair never occurred. But the same upheaval occurred again in stock bottles. Moreover, the individual steps were found over and over again in controlled matings either of px bl or its derivatives, e.g., reverse mutation px to plus and again plus to px, plus to different svr^{poi} alleles, or one allele into another, alone or simultaneously, with mutation to bran or one of its alleles, return mutation from both to plus, mutation at the bs locus, aside from a relatively high frequency of other mutants. The details, to be described below, completely exclude any idea of experimental error.

III. ANALYSIS OF THE px bl STOCK AND THE MUTANTS IN THE REGION OF THE PRIMARY CHANGES (svr, px, bs, a)

Whatever may be the genetical basis of the briefly described primary mutational changes, the only hope for gaining an insight is to elucidate as completely as possible the genetic constitution of the original px bl line and of the stocks of mutants at the loci found to mutate rather frequently, whether they are derived from the original line directly or indirectly. We propose to present first the data for the mutants and afterward those for the px bl stock.

1. The Basic Recurrent Mutants

a. the mutant pointed, svr^{poi} (abbr.: poi)

Phenotype.—Pointed looks like an exaggerated silver. It is still paler (comparison with two Pasadena stocks) and the wings are more pointed. In svr the pointed wing is not visible in mass cultures and not very distinct in pair cultures, though it comes out better when svr is extracted from crosses. In svr^{poi} it is always clear, more extreme in the females and also more typical in pair cultures. The body color is best described in comparison with others (as overleaf).[2]

[2] I owe this description to my former assistant, Dr. C. A. Villee, I myself being partly color-blind.

Oregon: grayish, yellow tinged with orange
svr^{poi}: light yellow, neither gray nor orange
sp^2: dark yellow-gray; abdomen, olive green tinge

The yellow of svr^{poi} is pale, whitish, not the lemon yellow of the yellow mutant. The bristles are always dark but tend to be softer than usual. Newly hatched flies are yellower than older ones. Also, the pigmentation of the testis is yellow (dark in wild type). One of the characteristics of standard silver is the presence of a dark trident upon the thorax (which is highly modifiable in expression); this is absent in pointed and its alleles. However, in a line made up to contain white (w) together with pointed the trident appears. Pointed has, further, an inclination toward soft wings (see below) and toward spreading of the wings, but more so in other alleles to be described.

Suppressor action.—Pointed acts as a suppressor for speck, but not for vermilion (for sable see below). As a rule, sp/sp, svr^{poi} in males shows no speck at all, but sp/sp, svr^{poi}/svr^{poi} females vary from no speck to an intermediate condition (which appears only as a very rare exception in males). Tests made with the available svr stocks never showed such a suppressor action. Pointed thus combines the action of silver and the near-by located suppressors; we shall return to this later in our discussion.

One remarkable detail ought to be added. If flies are made up with speck opposite a speck deficiency, and pointed in the first chromosome, they are pointed and speck. The suppressor action is inferior to the enhancing action (exaggeration) of the deficiency, a fact of considerable interest for phenogenetical deliberations.

As sp suppression by the specific suppressors said to be located near svr usually entails sable suppression also, a check for s^2 was made. Crossover flies containing in the same chromosome pointed and sable forked were less dark than sable, and the dark trident which is very typical for s^2 was about one-third lighter than in the s^2 brothers without poi. Pointed thus is also a part suppressor for sable. This, by the way, represents a rather complex phenogenetical situation: svr has a trident; svr^{poi} not, but has it in the presence of w; but the sable trident is partly suppressed by svr^{poi}. The speck suppression also has its modifiers. If the entire X chromosome of pointed to the right of this locus is replaced by crossing over—w was used as a marker,—sp is only half suppressed in the males.

Localization.—Compounds svr^{poi}/svr are always pale but do not always show the pointed wing tip; however, as a whole they appear as expected if pointed is a silver allele. In heterozygotic condition svr^{poi} sometimes shows a very slight dominance effect of the pointed feature, which must be due to modifiers. Genetic localization was not easy, because crossing over in the tip of the first chromosome is known to be unreliable. For example, in tests of the y–w region in one experiment there were only 3 crossover males among more than 800 males and all these three were yellow, not pointed. In another experiment with the same loci, 499 ♀ 417 ♂ noncrossover, 3♀ 3 ♂ y 3 ♀ 2 ♂ w, both not pointed, were obtained. Thus pointed did not show with one of the loci, but crossing over was reduced in this region, though not by much. But later the visible crossover combination with w was obtained, though never with y.[8] Another experiment with prune (pn 0.8) gave no crossovers among

[8] K. Brehme (Proc. Nat. Acad. Sci. Wash., 27 [1941], 254–261) states that the combination y with svr is lighter than either alone. We never succeeded in finding the combination with svr^{poi}.

almost 1,300 flies; kurz (1.7) gave no crossovers with 700 flies; with sc ec only 3 scute not ec (and no ec not sc) males were found among nearly 1,300 flies, some of them pointed. Obviously, y does not permit pointed to express itself. This might be a consequence of the fact that both loci control a body color, thus y being epistatic over svr^{poi}, including the pointed wing effect. Some of the other crossover recombinations were not reliable phenotypically. The experiments were later repeated with a selected poi stock which showed the character very clearly, and crossovers were found. Table 2 presents the results.

The first two tests give a locus between 0.6 and 0.7. The fa test has a value to the right of fa, but as fa is not easily classified the result is hardly reliable. The ec test puts poi to the left of w. Actually the poi crossover class appears much smaller than the reciprocal one, probably because of poor expressivity; sex-linked lethals in the poi chromosome which can be responsible will, however, be described later. If we calculate only on the basis of the plus class, the value becomes 0.1 for the

TABLE 2

LOCALIZATION OF SVR^{poi}

	Number of flies	C.o.	Per cent	Locus of marker	Reciprocal c.o. classes	
					+	poi marker
C.o. poi–pn^2	1357	2	0.14	0.8	..	2
C.o. poi–w	852	7	0.81	1.5	6	1
C.o. poi–fa	675	36	5.06	3.0	20	16
C.o. poi–ec	938	41	4.19	5.5	27	14
					53	33

experiment with w, and zero with ec. Silver is located at 0.1. For a long time we had assumed that poi is a translocation of the ll sp loci into the first chromosome to the left of white, because an insertion of 2–3 bands was found here in the salivaries and the crossover values with ec could be interpreted in favor of this (also the sp suppression). But later tests showed the sp suppressor action to be independent of a duplication and in the nature of other suppressor actions in that region, and the compound actions showed that poi must be a silver allele. The decisive check is obtained by crossing pointed to L. V. Morgan's deficiency and duplication 101, which is deficient for the left end of X including silver. Silver × Df 101 was used as control. Actually, the heterozygous deficiency effect (without exaggeration [once a compound svr/Df showed exaggeration]; also in svr) was found—with decreased viability,—thus proving that pointed is covered by the deficiency and actually is a silver allele. But this is not the whole story, as will be shown later in an analysis of the X chromosomes of the silver group and in a discussion of the features of this region. The translocation which first was suspected is much farther to the right, beyond facet.

An independent allele of pointed—Independently of the present work we found an allele of pointed which closely resembles this, though there are a few differences. It was found in the offspring of heat-treated flies and had been isolated as a sex-linked recessive, indistinguishable from the present pointed wing except that the

pointed wing tip is usually better expressed in this mutant. The pedigree of this mutant poi h (h for heat) is:

F_1 ♀♂ Oregon, heat-shock shortly before pupation: 12 ♀♀, 9 ♂♂ +
$F_2 = F_1$ Mass: 213 ♀♀, 233 ♂♂, 1♂ notched
R F_3 = Oregon ♀ × notched ♂ F_2: all +, but 1 ♂ notched and poi
F_4 Mass F_3 +: 400 ♀ ♂ +, 19 ♂♂ poi

In crosses they behaved as alleles, but they are in some respects, apart from the pointed phenotype, genetically different, as will be shown below. We shall call the latter mutant $svr^{poi\ h}$ (abbr.: poi h.)

Expressivity.—The expressivity of the phenotype of pointed is important for our later discussion of its origin. The pale body color and the suppression of speck is always clear, though in the presence of plexus the body color is not always distinctive. But the pointed wings are rather variable, except in selected stock, though less so than in silver. It turned out that our selected stock of svr^{poi} and also of $svr^{poi\ h}$ contained definite dominant modifiers. (We have already seen that yellow [y] prevents the expression of pointed wings; but this might be called an epistatic action.) They first became clearly visible in translocation tests, i.e., y, bw, e, ey ♀ × (y, bw, e, ey × poi) ♂. In the F_1 different results had already appeared. Sometimes all the sons of y × both pointed alleles were clearly pointed; sometimes the character appeared intermediate, with a varying number of soft and spread wings (which is an irregular feature of the pointed phenotype and especially of certain alleles; see below); sometimes the males might have passed for normal. The backcross behaved in the same way, and there also appeared a relation between the expressivity and the autosomal recombinations. The same features were observed for sons of pointed mothers and other fathers. On table 3 a series of such crosses was checked for the expressivity of pointed in three grades A, B, C (also for sex ratios; see below). The considerable variability becomes evident, which in this case must be based upon the presence of modifiers in the stock used for crossing. Actually, some of the series are rather consistant, e.g., a sp crosses: always full expression; y w crosses: medium; bw sp ba crosses: poor expression. The column "Remarks" shows that frequently the pointed F_1 males are also soft or soft and folded.

There is, further, a considerable inclination toward spread wings, which characterizes also lanceolate (ll), i.e., a similar phenotype at a different locus. In one case ½ of the males were more or less blistered. Here the balloon locus was involved (actually a mutant bran had appeared); we shall return to this case. It is remarkable that one blistered female appeared in one of the Lausanne crosses, as we had found (see below in chapter on blistering) that the Lausanne stock of wild flies tends to show blistered wings.

We now compare these data with some for the allele $svr^{poi\ h}$, which is not related to px bl and svr^{poi}. Table 4 registers these data. We notice that as a rule the pointed character of the males is much better expressed than in the crosses with svr^{poi}. Unclassifiable or actually not pointed males do not occur. (But this does not apply to F_2; see below.) It was frequently noted that the character was best expressed in broods with a low sex ratio. Only rarely do soft males appear, but they are found, thus showing that this allele also has the same tendency, though a lower one, to produce soft wings. A very frequent occurrence is females and, more rarely, males with abnormal abdomen. In the C series there are a few in almost every brood.

TABLE 3

svr^{poi} ♀ × N ♂

(Grades of pointed: A, type; B, intermediate; C, poor)

No.	Father	♀	♂	Grade of pointed ♂	Remarks	Sex ratio n ♀ : 1 ♂
5682 B	triple	74	36	A	.....	2.1
5705 B	X ple	75	39	B	Most ♂ soft folded.....	1.9
5710 B	ey	57	37	A	Most ♂ soft folded	1.5
6197	5 ple	121	47	A	1 ♂ spread.....	2.6
6289 B	Lausanne	18	10	A, B	.....	1.8
6290 B	Lausanne	127	68	A, B	1 ♀ blist.....	1.9
6291 B	Lausanne	114	43	A, B	.....	2.6
6320 B	px bw sp	96	31	A, B	.....	3.1
6322 B	a sp	24	2	A	.....	12.0
7824 B	a sp	111	92	A, 2 ♂ +	.....	1.2
7825 B	a sp	115	69	A	.....	1.7
2826 B	a sp	119	57	A 4 ♂ ?	.....	2.1
7827 B	a sp	86	54	A	.....	1.6
7828 B	a sp	115	84	A 2 ♂ ?	.....	1.4
7829 B	a sp	70	36	A	.....	1.9
7831 B	a sp	118	69	A	.....	1.7
3061 C	y w	52	57	B	Many spread.....	0.9
3062 C	y w	39	44	B	Many spread.....	0.9
3064 C	y w	74	62	B	Many spread.....	1.2
3070 C	y w	15	15	B	Many spread.....	1.0
3082 C	bw sp ba	48	17	C	.....	2.8
3083 C	bw sp ba	65	42	C	Some spread.....	1.5
3084 C	bw sp ba	59	46	C	.....	1.3
3085 C	bw sp ba	57	35	C	Half ♂ also soft and spread blistered	1.6
3086 C	bw sp ba	36	27	C	.....	1.3
3087 C	bw sp ba	93	46	B, C	Many ♂ soft.....	2.0
3088 C	bw sp ba	84	61	B, C	Many ♂ soft.....	1.4
3089 C	bw sp ba	45	31	B, C	Many ♂ soft.....	1.4
3090 C	bw sp ba	75	59	B, C	Many ♂ soft.....	1.3
3107 C	b j p	54	47	B	.....	1.1
3124 C	triple	66	57	B	.....	1.2
3125 C	triple	88	96	B	Most ♂ soft folded.....	0.9
3126 C	triple	135	84	A, B	.....	1.6
3128 C	triple	84	58	B	Most ♂ soft folded.....	1.4
3129 C	triple	84	52	A, B	.....	1.6
3131 C	triple	127	97	A, B	.....	1.3
3132 C	triple	125	77	A, B	.....	1.6
3147 C	y a c	136	71	A	.....	1.9
3148 C	y a c	102	72	A	.....	1.4
3149 C	y a c	80	71	A, B	.....	1.1
3163 C	ec ct g	34	19	B, C	.....	1.8
3164 C	ec ct g	34	28	B, C	.....	1.2
3165 C	ec ct g	45	33	B, C	.....	1.4
3166 C	ec ct g	46	33	A, B	.....	1.4
3167 C	ec ct g	14	25	A, B	.....	0.6
3171 C	ec ct g	76	52	A, B	.....	1.5
3172 C	ec ct g	21	14	A, B	.....	1.5
Sa.		3533	2302		.....	1.5
Avg.		75	49			

TABLE 4

svr^{poi} × N ♂

No.	Father	♀	♂	Grade of pointed ♂	Remarks	Sex ratio n ♀ : 1 ♂
5662 B	5 ple	62	25	A B	11 ♀ 2 ♂ abnormal abdomen (not inherited)	2.5
5663 B	5 ple	55	12	A B	4 ♀ 1 ♂ abnormal abdomen	4.6
5699 B	X ple	95	69	A		1.3
5701 B	triple	31	9	A	♂ soft	3.4
5702 B	triple	35	25	A B		1.4
6424 B	X ple	113	52	A B		2.2
6168 B	5 ple	96	11	A		8.7
6169 B	5 ple	119	37	A		3.2
6170 B	5 ple	41	5	A		8.2
6171 B	5 ple	82	4	A		20.5
6172 B	5 ple	125	43	A		3.0
3071 C	y w	27	28	A B		1.0
3072 C	y w	63	33	A	Pointed character more marked where fewer males	1.9
3073 C	y w	23	22	A B	In all the crosses series C frequently ♀ with abnormal abdomen	1.0
3075 C	y w	81	55	A		1.5
3076 C	y w	41	27	A		1.5
3077 C	y w	66	33	A		2.0
3078 C	y w	51	25	A		2.0
3079 C	y w	65	51	A B		1.3
3080 C	y w	54	42	A B		1.3
3091 C	bw sp ba	120	76	A B		1.6
3092 C	bw sp ba	29	26	A B		1.1
3093 C	bw sp ba	94	72	A B		1.3
3094 C	bw sp ba	35	7	A B		5.0
3095 C	bw sp ba	110	74	A B		1.5
3097 C	bw sp ba	23	35	A B		0.7
3098 C	bw sp ba	94	55	A B		1.7
3099 C	bw sp ba	74	56	A B	1 ♂ spread blistered	1.3
3100 C	bw sp ba	14	5	A B		2.8
3114 C	b j p	39	37	A B		1.1
3115 C	b j p	38	14	A B		2.7
3116 C	b j p	13	12	A		1.1
3117 C	b j p	85	54	A B		1.6
3118 C	b j p	28	10	A B		2.8
3119 C	b j p	30	13	A B		2.3
3121 C	b j p	75	65	A B		1.1
3122 C	b j p	98	73	A B		1.3
3133 C	triple	109	97	A B		1.1
3135 C	triple	93	88	A B	Many ♂ soft folded	1.1
3136 C	triple	72	45	A		1.6
3137 C	triple	50	40	A B		1.3
3138 C	triple	111	107	A B	Many ♂ soft folded	1.0
3139 C	triple	91	56	A		1.6
3140 C	triple	91	71	?		1.3
3141 C	triple	89	44	A		2.0
3142 C	triple	140	124	A B		1.1

TABLE 4—(*Continued*)

No.	Father	♀	♂	Grade of pointed ♂	Remarks	Sex ratio n ♀ : 1 ♂
3153 C	y a c	109	68	A B	.....	1.6
3154 C	y a c	131	76	A B	.....	1.7
3155 C	y a c	112	83	A B	.....	1.4
3156 C	y a c	116	98	A B	.....	1.2
3157 C	y a c	111	60	A B	.....	1.8
3158 C	y a c	88	80	A B	.....	1.1
3159 C	y a c	25	29	A B	.....	0.9
3160 C	y a c	68	85	A B	.....	0.8
3161 C	y a c	93	54	A B	.....	1.7
3162 C	y a c	96	56	A B	.....	1.7
3173 C	ec ct g	109	93	B	.....	1.2
3174 C	ec ct g	121	72	A	.....	1.7
3175 C	ec ct g	92	74	A	.....	1.2
3178 C	ec ct g	101	74	A B	.....	1.4
3179 C	ec ct g	77	67	B	.....	1.1
3180 C	ec ct g	101	90	B	.....	1.1
Sa.		4700	3122		.....	1.5
Avg.		76	51			

Many have been tested, and the character was never inherited. But we shall later see that a genetic type of abnormal abdomen is obtained from poi involving the bb locus.

The modification of expressivity just recorded is of minor significance. But there is another, more important, one which became visible in F_2 and backcrosses, in which half the males or females and males ought to be pointed. Table 5 contains a series of reciprocal F_2 for both alleles with Oregon.

Looking at the summarized results, a few regularities become visible: (1) Never is the ratio +: poi the expected 1:1 in either set (checking only the wings, not the pale color; see below: viability). (2) Where both sexes contain pointed flies the ratio for females is much higher than for males. In both these cases the sex ratio is normal, the ratio of + ♀ : + ♂ is also normal, and therefore about the same number of genetically pointed individuals do not exhibit the character in both sexes. In the $svr^{poi\ h}$ crosses, however, there are still more males which do not show the character. In the average here, a little more than ½ of the females homozygous for poi, but about ⅔ of the males, no not show the character. This suggests that a recombination with two or three dominant enhancers introduced from the poi stock may be responsible for the lack of expressivity of pointed. (3) The reciprocal crosses in which the poi-containing first chromosome was introduced by a poi father are different. First, the sex ratio is a very high one, about ⅓ of the males missing (see below). The proportion of males exhibiting pointed is only about ⅛ of all the males. The ratio of + ♀ : + ♂ is 1.7 :1. If we assume that just as many poi males are phenotypically plus as in the reciprocal cross, we can subtract these from the plus males. The ratio was 17 : 10 in the opposite cross, which means that in the present cross about 170 males in the plus class are supposed to be genetically pointed. Subtracting these, the ratio 2 ♀ : 1 ♂ + is approximately realized. From this it follows that between ½ and ⅝ of the poi males are lethal. In other words, the X chromosome, if introduced

by a poi male, contains something which is lethal in connection with about 5 out of 8 autosomal recombinations; this problem will be studied below. (4) The individual ratios are arranged so as to give information on whether different grandparents of the same cross may have a specific influence (the number of F_1 means always one

TABLE 5

RECIPROCAL F_2 OF svr^{poi} AND $svr^{poi\,h}$ WITH WILD TYPE 7145/73 Br.

No.	Cross	+		poi		Soft folded		Ratio ♀:1♂	Ratio +:poi		Ratio +♀:+♂
		♀	♂	♀	♂	♀	♂		♀	♂	
7145	$(svr^{poi} \times Ore)^2\ 7079^2$.....	69	59	17	..	..	16	1.1	4.0	3.7	1.2
7146	$(svr^{poi} \times Ore)^2\ 7079^2$.....	82	87	25	4	..	9	1.1	3.3	6.7	0.9
7147	$(svr^{poi} \times Ore)^2\ 7079^2$.....	56	47	9	..	22	32	1.1	1.8	1.5	1.2
7148	$(svr^{poi} \times Ore)^2\ 7079^2$.....	47	62	31	13	..	..	1.0	1.5	4.8	0.8
7149	$(svr^{poi} \times Ore)^2\ 7081^2$.....	59	63	13	2	13	17	1.0	2.3	3.3	0.9
7150	$(svr^{poi} \times Ore)^2\ 7081^2$.....	71	73	22	5	1	2	1.2	3.1	10.4	1.0
7151	$(svr^{poi} \times Ore)^2\ 7081^2$.....	87	64	15	6	9	25	1.2	3.6	2.1	1.4
7153	$(Ore \times svr^{poi})^2\ 7082^2$.....	103	91	..	7	..	..	1.1	...	13.0	1.1
7154	$(Ore \times svr^{poi})^2\ 7082^2$.....	116	75	..	4	..	11	1.3	...	4.0	1.6
7156	$(Ore \times svr^{poi})^2\ 7083^2$.....	120	78	..	8	..	3	1.3	...	7.0	1.5
7157	$(Ore \times svr^{poi})^2\ 7084^2$.....	77	52	..	..	..	..	1.5	...	...	1.5
7158	$(Ore \times svr^{poi})^2\ 7084^2$.....	82	34	..	..	..	..	2.4	...	...	2.4
7159	$(svr^{poi\,h} \times Ore)^2\ 7088^2$	88	81	..	13	..	..	0.9	...	6.0	1.1
7160	$(svr^{poi\,h} \times Ore)^2\ 7088^2$.....	77	92	14	5	..	..	0.9	5.5	18.0	0.9
7161	$(svr^{poi\,h} \times Ore)^2\ 7088^2$.....	85	88	32	9	..	..	1.2	2.7	9.8	1.0
7162	$(svr^{poi\,h} \times Ore)^2\ 7088^2$.....	69	78	30	8	..	..	1.2	2.3	9.7	0.9
7163	$(svr^{poi\,h} \times Ore)^2\ 7088^2$.....	97	109	22	6	..	..	1.0	4.5	18.0	0.9
7164	$(svr^{poi\,h} \times Ore)^2\ 7089^2$.....	116	122	12	..	6	21	0.9	6.4	6.0	1.0
7165	$(svr^{poi\,h} \times Ore)^2\ 7089^2$.....	106	122	17	5	..	5	0.9	6.2	12.2	0.9
7167	$(Ore \times svr^{poi\,h})^2\ 7090^2$.....	161	87	..	14	..	..	1.6	...	6.2	1.9
7168	$(Ore \times svr^{poi\,h})^2\ 7090^2$.....	135	82	..	13	..	..	1.4	...	6.3	1.6
7169	$(Ore \times svr^{poi\,h})^2\ 7091^2$.....	138	67	..	11	..	..	1.8	...	6.1	2.1
7170	$(Ore \times svr^{poi\,h})^2\ 7091^2$.....	124	52	..	17	..	..	1.6	...	3.1	2.4
7171	$(Ore \times svr^{poi\,h})^2\ 7092^2$.....	141	89	..	7	..	..	1.5	...	12.7	1.6
7172	$(Ore \times svr^{poi\,h})^2\ 7092^2$.....	119	79	..	9	..	..	1.4	...	8.8	1.5
	All $(svr^{poi} \times Ore)^2$.....	471	455	132	30	45	101	1.1	2.7	3.5	1.0
	All reciprocal.....	498	330	...	19	..	14	1.4	...	10.0	1.5
	All $(svr^{poi\,h} \times Ore)^2$.....	638	692	127	46	6	26	1.0	4.8	9.6	0.9
	All reciprocal.....	818	456	...	71	..	..	1.6	...	6.4	1.8
	All grandmother poi.....	1109	1147	259	76	51	127	1.1	3.6	5.7	1.0
	All grandfather poi.....	1316	786	...	90	..	14	1.5	...	7.6	1.7

pair mating, and different numbers, different pairs). There are two sister F_2 7157, 58 without pointed males; but this is not significant in this group. There are twice (7164–65, 7171–72) sister broods with higher poi ratios than the others in the group; but this is not necessarily significant.

The best method for checking upon the supposed enhancers is to cross pointed to y, bw, e, ey, and F_1 males back to y, bw, e, ey ♀, the standard translocation test. (Patterson test). All sons from these crosses have the poi X chromosome with different autosomal recombinations: either heterozygous for one or the other of the poi autosomes, or homozygous for foreign chromosomes. If F_1 had all pointed males

(which is not always the case; see above), all the dominant enhancers are present in the heterozygote and the backcross must give information.

We have mentioned already that, in F_1 y × both alleles, all males are sometimes clearly pointed and sometimes not. As an example table 6 may serve. Many other crosses gave the same results, namely, sometimes the F_1 males are clearly pointed, all of them or some of them; sometimes pointed is not clear at all, and sometimes it cannot be distinguished. (This means only the wing shape, not the pale color.) But whenever these males were backcrossed to pointed females they turned out to be genetically pointed, siring only pointed offspring. The other features, such as appearance of soft folded and spread males and the varying sex ratios, are the same as in ordinary crosses, and the males which did not exhibit pointed wings were pale.

In a large backcross series with y, bw, e, ey, involving 17 with svr^{poi} and 6 with

TABLE 6

F_1 y × pointed (Patt = y, bw, e, ey)

No.	Mother	Father	♀	♂ point	♂ ± point	♂ ± no	Remarks
5755	Patt	svr^{poi}	48	21	21	..	
5762	Patt	svr^{poi}	36	15	..	..	12 ♂ soft folded
5853	y	svr^{poi}	76	60	..	19	4 ♂ spread
6193	Patt	svr^{poi}	28	..	..	12	
6223	Patt	$svr^{poi\,h}$	22	..	8	..	
6224	Patt	$svr^{poi\,h}$	15	..	7	..	
6225	Patt	$svr^{poi\,h}$	23	..	14	..	
Sa.	....	.....	248	..	193	..	

$svr^{poi\,h}$ and about 800 ♂, it was found consistently that all plus males were typically pointed, also all eyeless males. All brown males with or without eyeless were about intermediate; all ebony males, with or without eyeless, were very little pointed; and males both ebony and brown, with or without eyeless, were to all purposes normal. This shows that "dominant" modifiers for wing shape are present in the second and third chromosomes of pointed, and the more powerful ones in the third. It may be of interest in this connection that the pointed wing develops from a wing completely normal at the time of pupation (Goldschmidt, 1937*a*), the histological events being unknown. One should expect that a character fixed so late in development would be likely to respond easily to modifying action, genetic and otherwise.

Heterozygous effects.—In the F_1 crosses with marked stocks another feature was found regularly. In crosses of svr^{poi} with stocks containing ebony, alone or in combination with other markers, a dominance effect was observed which first suggested a deficiency but did not turn out to be one. The effect is rather irregular, sometimes hardly observable, sometimes found in all females and males, which look like the ebony allele sooty. Sometimes even a part of the flies, especially males, look like a weak ebony with dark wings in addidtion to the body color. Table 7 contains some of the notes. The table shows clearly the dominance shifting effect of svr^{poi} for ebony. As the effect appears in crosses in both directions and therefore also in males without the svr mutant in the X chromosome (and also in backcrosses), it is autosomal in nature and may be due actually to the e locus of svr^{poi}. The allele $svr^{poi\,h}$, however, never produces this effect, which, then, is clearly derived from the px bl stock but

must be connected with the mutation to svr^{poi}, as it is not found in the px bl line. Rudimentary, which was produced together with pointed, shows the same effect! The difficulty of classification and the variability of the effect did not permit a direct localization (see below: third chromosome tests). It has already been mentioned that silver tends to show a trident on the thorax, shining through the pale cuticle. The pointed alleles never exhibit a trident. The e effect has nothing to do with this feature of the svr locus, as neither the heterozygote with black, nor compound with

TABLE 7

CROSSES INVOLVING pointed AND ebony

(Color grades: I, weak trident and normal; II, trident; III, sooty; IV, low ebony)

No.	Cross	Color	Remarks
6173 B	svr^{poi} × triple....	Part ♀♂ III.....	Some ♀♂ ski wings, with and without III. 5 ♀ blist
6174 B	reciprocal.....	All II, III.....	Many ski wings
6448 B	triple × $svr^{poi\,h}$...	All normal.....	
6450 B	triple × $svr^{poi\,h}$...	All normal.....	
6501 B	triple × $svr^{poi\,h}$...	All normal.....	
6512 B	triple × $svr^{poi\,h}$...	All normal.....	
6478–86 B	$svr^{poi\,h}$ × triple...	7 broods normal.....	
6487 B	svr^{poi} × triple....	II.....	
6488 B	svr^{poi} × triple....	II.....	
6489 B	svr^{poi} × triple....	II.....	
6490 B	svr^{poi} × triple....	II, III.....	
6491 B	svr^{poi} × triple....	II.....	
6493 B	svr^{poi} × triple....	II.....	
6494 B	triple × svr^{poi}....	II–IV (about ½ ♀♂ IV)	
6495–98 B	triple × svr^{poi}....	3 broods all III and IV..	
6500 B	triple × svr^{poi}....	II.....	
6426–44 B	triple × (triple × svr^{poi}) ♂ III–IV	All not triple II–III....	

silver, shows the trident. We anticipate that we shall find evidences for a rearrangement in the e region so that the heterozygous effect might be actually a position effect.

The same mutant produces other dominance-shifting effects. In crosses with second-chromosome markers the locus arc is frequently semidominant. For example, in no. 6280 quintuple × svr^{poi}, out of 42 ♀ 46 ♂, there were 14 ♀ 7 ♂ more or less arc, but none perfect. Again, deficiency tests failed and the irregularity was the same as for ebony. The number of individuals showing the dominance effect was always small. Furthermore, this effect was not typical for svr^{poi}, but was also found in the allele $svr^{poi\,h}$. It was clearly related to the action of the svr locus, as only pointed females and males showed the effect, not the heterozygous females. We remember at once that bran is an arc allele and that svr^{poi} tends to produce bran as a mutant. Again the possibility of a position effect with a disturbance at or near the arc locus is suspected (see below).

There is a third similar effect, more interesting than the two just described. In a series of crosses with both silver alleles and the first-chromosome locus achete, in a majority of broods about one-half of the females were achete, though the character

was again less clearly expressed than in the pure achete stock, and more variable. Many tests were made to clear up this effect, as the silver locus is located not so far away from yellow and achete, and as it was frequently observed that svr^{poi} individuals, especially males, tended to have a light yellowish (lemon) tinge, besides being pale. (The mutant achete, by the way, had originated in all individuals of a

TABLE 8

BRISTLES IN SVR CROSSES

No.	Cross	♀	♂	Bristles
3696 C	$poi^{px\,bl} \times Inv(1)y^{px\,bl}$....	111	95	d.c.p. 12 ♀
3697 C	$poi^{px\,bl} \times Inv(1)y^{px\,bl}$....	109	50	50 ♀ 26 ♂ bb.
3698 C	$poi^{px\,bl} \times Inv(1)y^{px\,bl}$....	30	28	+
3710 C	$poi \times Inv(1)y^{px\,bl}$.....	60	33	6 ♀ d.c.p.
3711 C	$poi \times Inv(1)y^{px\,bl}$.....	73	64	22 ♀ d.c.p.
3713 C	$poi^{px\,bl} \times y\ ac$.....	97	?	Little bb.
3714 C	$poi^{px\,bl} \times y\ ac$.....	100	53	+
3715 C	$poi^{px\,bl} \times y\ ac$.....	128	90	1 ♀ d.c.p.
3716 C	$poi^{px\,bl} \times y\ ac$.....	112	67	+
3717 C	$poi^{px\,bl} \times y\ ac$.....	83	52	7 ♀ d.c.p., 1 also d.c.a.
3873 C	poi × Ore.....	97	28	All ♀ much bb, ½ ♂ bb.
3874 C	poi × Ore.....	100	95	All ♀ ♂ bb.
3875 C	poi × Ore.....	135	60	½ ♀, few ♂ d.c.p.
3876 C	poi × Ore.....	116	79	Almost all bb.
3877 C	poi × Ore.....	120	77	Almost all ♀, about ½ ♂ bb.
3878 C	$poi^{px\,bl} \times$ Ore.....	138	75	15 ♀ d.c.p.
3879 C	$poi^{px\,bl} \times$ Ore.....	154	82	All ♀, few ♂ bb.
3880 C	$poi^{px\,bl} \times$ Ore.....	91	54	Almost all bb.
3881 C	$poi^{px\,bl} \times$ Ore.....	138	69	Almost all ♀, few ♂ bb.
3881 C	$poi^{px\,bl} \times$ Ore.....	100	96	½ ♀, few ♂ bb.
3812 C	3696^2 ♀ d.c.p.....	78	87	All +, many similar F_2 bb or only few d.c.p.
3843 C	$3697 \times Inv(1)\ y^{px\,bl}$.....	131	145	♀ y 48 + 31 bb ♂ poi 50 + 10 d.c.p. ♀ not y 30 + 22 d.c.p. ♂ y 55 + 33 bb.
3844 C	$3697 \times Inv(1)\ y^{px\,bl}$.....	...	...	Only few ♀ y d.c.p. others and ♂ +
3861 C	3710^2 ♀ +.....	...	...	Most ♀ few ♂ all classes bb.
3862 C	3710^2 ♀ d.c.p.....	...	...	½ ♀ poi or not poi d.c.p. ♂ +
3863 C	3711^2 +.....	...	...	½ ♀ ♂ poi or not c.d.p.
3864 C	3711^2 ♀ d.c.p.....	...	...	All ♀, ½ ♂ both classes bb.

yellow brood.) A repetition of the cross yielded 12 broods without an achete effect and 2 with a slight effect. This led to a closer investigation. Repeated checks of cultures of both svr alleles always showed normal bristles, even comparatively long ones. But in the majority of crosses, F_1 and later generations, abnormalities are found, whatever the cross. The bristle effect turned out to be completely independent of the svr locus, and also of achete, and to be a purely autosomal effect connected with the poi mutation, as it is found in both alleles. (We shall see below that svr^{poi} frequently contains a bb allele without visible effects except in compounds. This bb allele is not involved in the present discussion). Table 8 contains some pertinent data for F_1. The crosses were made with: a small Inversion, to be described later as I (1) $y^{px\,bl}$, with one break in the y–ac region; with y ac standard stock; and with Oregon wild males. The results show a considerable variation:

normal bristles in F_1; only the posterior dorsocentrals (d.c.p.) affected, with one or both missing in females or in both sexes, and in a few or many individuals; occasionally, also, the anterior dorsocentrals affected (d.c.a.); some bristles shortened (phenotype as in bb), or more or all shortened to a condition resembling spineless. In this latter type the scutellars lead. This extreme effect may be found in all females and males, mostly in females or in part of them in many variations, as the table shows. There is no relation to the y or ac locus, as the Oregon crosses show even more of the effect than those with mutants or breaks in the y–ac region.

TABLE 9

FERTILITY EXPERIMENT

Cross	No. fertile	No. sterile	Fertility (per cent)
Ore-R ♀ × Ore R ♂	111	0	100.0
px bl ♀ × Ore R ♂	99	5	95.2
svr^{poi} ♀ × Ore R ♂	110	6	94.8
slender ♀ × Ore R ♂	97	8	92.3
$svr^{poi\,h}$ ♀ × Ore R ♂	95	11	89.7
T px ♀ × Ore R ♂	93	7	93.0
poi bl ♀ × Ore R ♂	97	3	97.0
px from poi ♀ × Ore R ♂	98	4	96.07
soft bl ♀ × Ore R ♂	94	7	93.06
Ore R ♀ × px bl ♂	101	7	93.5
Ore R ♀ × svr^{poi} ♂	98	2	98.0
Ore R ♀ × slender ♂	98	2	98.0
Ore R ♀ × $svr^{poi\,h}$ ♂	94	6	94.0
Ore R ♀ × T px ♂	99	1	99.0
Ore R ♀ × poi bl ♂	92	11	89.3
Ore R ♀ × px from poi ♂	97	8	92.3
Ore R ♀ × soft bl ♂	80	23	77.6

There is, further, no relation to the sex ratio, and though the males tend to show less of the effect, it is sometimes present in all males with the poi X chromosome. The lower part of the table contains some checks upon F_2. These show a corresponding irregularity. The X chromosome obviously does not influence the result, which must be based upon some autosomal condition acting and segregating in an irregular way. Actually, the absence of the poi X chromosomes seems to enhance the bristle effect, as, at least in some cases, the homozygous y Inversion flies were more like bb—which, however, may be a specific effect of this inversion (see below). F_3 from both poi and y F_2 flies, however, were again irregular; for example:

4494 = 3861² poi and bb-like: only 2 d.c.p. ♀ among 60 poi.
4495 = 3861² poi +: the same (all poi)
4496 = 3861² ♀ poi bb-like, ♂ poi; all ♀ (146) no, ♂ (104) d.c.p. (all poi)
4497 = 3861² ♀ ♂ y bb-like; ½ ♀ ♂ y bb-like, ½ +
4500 = 3861² ♀ ♂ y bb, ♂ y: ¼ ♀, few ♂ d.c.p.

Further trials to elucidate this situation were completely unsuccessful. When repeated about one and one-half years afterward, the effect did not reappear. Obviously the underlying condition had been selected out of the stock. Probably one of the deficiencies found in the salivaries was responsible.

Viability and fertility.—The viability is lower than in normal flies, the average number of flies in a single-pair bottle, *ceteris paribus,* being about one-half the number in controls, which, however, as we shall see, may be caused by the presence of lethal classes. Also the fertility is a little lowered, as table 9 shows, more so in the females. This table, compiled for some of the mutants and their recombinations with mutants at the px, svr, a loci (derived from px bl), is based upon the following experiment : 1 ♀ 2 ♂ of the respective combinations were left in a bottle at 25° C. On the sixth day, bottles were discarded in which there was not at least the female and one male alive. The remaining bottles were reëxamined on the tenth day and those

TABLE 10

PHENOTYPES (No. 5426 ff.)

No.	Compound	Phenotype
1	Px^1/ll sp	Exagg. sp; medium plexation; web and net in I (see terminology in section on px bl)
2	Px^2/ll sp	No sp; low plexation; only few extra veins and branch of cross vein
3	Px^1/bs	♀ Web at cross vein, all blistered; ♂ web; extra venation in II
4	Px^2/bs	♀ Web at cross vein mostly blistered, ♂ antler-web
5	Px^1/ba	Web at cross vein, periclinal vein, net in II, ♀ much blistered, many ♂ blistered
6	Px^2/ba	The same, but no ♂ blistered and less net
7	Px^1/+ ♀ svr^{poi}/+, ♂ svr^{poi}	Most ♀ ♂ low plexus more or less like Px^1/+ ! some normal; ♂ poi pale
8	Px^2/+ ♀ svr^{poi}/+, ♂ svr^{poi}	The same but less plexation; more or less like Px^2/+
9	bs/+ ♀ svr^{poi}/+, ♂ svr^{poi}	Normal like bs/+ with a little dominance effect in ♀ (EV)
10	ba/+ ♀ svr^{poi}/+, ♂ svr^{poi}	The same

without larvae were called sterile. The sex ratio was about normal in both lines, e.g., in one count 385 ♀ 339 ♂ = 1.1 : 1 for svr^{poi}, the greatest individual deviation in favor of females being 77 : 55. For $svr^{poi\ h}$ the count was 496 ♀ 441 ♂=1.1 : 1, the greatest deviation in favor of females being 55 ♀ : 36 ♂.

Pointed and lanceolate (ll).—Pointed wings look exactly like lanceolate wings (ll, 2d chr.), though lanceolate is not pale and has no suppressor action. A combination of a higher allele of pointed with a bran allele, called slender, looks exactly like ll^s. Also both have a tendency to spread their wings. This might be just a phenotypical resemblance. At the time when I thought that pointed is a speck duplication (because there is a small translocation near facet in the pointed stock) many experiments were performed to check upon the relation of ll and poi. F_1 between the two is completely normal, but in F_2 and backcrosses strange ratios appeared, based upon a lethal combination (see below). But when ll could be recombined with pointed it was typical (while sp, in the combination ll sp/ll sp ; svr^{poi} was suppressed as always in the presence of poi. Lanceolate, then, is epistatic in this combination.

Pointed and blistered, and balloon.—The origin of pointed from px bl involved the disappearance of blistered contained in px bl. On the other hand, pointed itself produces blistering if combined with the second-chromosome arc allele bran. There-

fore a check is needed to ascertain whether pointed shows any special interaction with blistered (bs) or the near-by and similar balloon (ba), or whether it contains a bs allele without visible effect except in the presence of a mutant at the arc locus.

No trace of the extra veins characteristic of these stocks (bs, ba) was ever found in pointed. A simple test such as the one performed with ll sp was not promising, on account of the phenotypic difficulties offered by the mutants bs and ba and their heterozygotes. (See discussion of this subject in the section on px bl.). These difficulties could be evaded by using bs and ba in the exaggerated condition shown in the presence of the Plexate deficiencies. (For a detailed description of all these phenotypes see the section on px bl.) The procedure was the following: the Plexates—deficiencies for bs, ba (sp)—were crossed to both pointed alleles, ll, bs, and

TABLE 11

EXPECTATION FROM (poi × bs) × (poi × Px^1)

	2d chr.	1st chr.	Phenotype without interaction poi–bs
⅛	bs/+	♀poi/poi	Like no. 9, table 10
⅛	bs/+	♀poi/+	Like no. 9, table 10
⅛	bs/Px^1	♀poi/poi	Like no. 3, table 10
⅛	bs/Px^1	♀poi/+	Like no. 3, table 10
⅛	Px^1/+	♀poi/poi	Like no. 7, table 10
⅛	Px^1/+	♀poi/+	Like no. 7, table 10
⅛	+/+	♀poi/poi	Normal
⅛	+/+	♀poi/+	Normal

ba; and both pointed alleles were crossed also to bs, ba to check again upon the phenotypes. (Px^1 includes sp, Px^2 does not.) Table 10 describes these phenotypes, which are classifiable without any difficulty.

Now F_1 svr^{poi} or $svr^{poi\ h}$ × bs was crossed with F_1 svr^{poi} or $svr^{poi\ h}$ × Px^1; the expectations from the combination (poi × bs) × (poi × Px^1) are shown in table 11. The decisive group is the one with bs/Px^1; which is expected to contain (one-fourth of the offspring) flies with much plexation with web and blisters, a type absent in all other combinations, which are less conspicuous and near normal. Also, the females of these two groups would be one-half pale, that is, homozygous poi, and one-half heterozygous.

The actual result for svr^{poi} was (nos. 5505 and 5506):

110 ♀ 116 ♂ normal or almost normal types
19 ♀ 20 ♂ Px^1/bs (blistered) type
18 ♀ 10 ♂ pointed, more plexus than first groups, no web, antler, or blisters.

This shows that homozygous pointed weakens the exaggeration effect of Px/bs.

The same test made for $svr^{poi\ h}$ (not derived from px bl) gave clearly ¼ of the Px^1/bs type and no interaction of the two loci; F_3 tests confirmed the result. Parallel crosses with Px^2 gave the same results as those with Px^1. Finally, also the corresponding combination with the compound svr^{poi}/$svr^{poi\ h}$ was built up. Actually (no. 5510), all individuals bs/Px^1 with the compound were blistered, etc., which confirms the difference found between the two pointed with a dominant action of $svr^{poi\ h}$.

A similar test for balloon was made simpler, because balloon was used with near-by speck; as Px^1 is a deficiency also for sp, all Px^1/sp ba individuals show speck. The very extreme plexate and blistered type of this compound is described in table 10, no. 5. The cross (poi × Px^1) × sp ba contains the answer (no. 5511):

not sp (i.e., not Px^1/sp ba) 38 ♀ 42 ♂ (½ ♂ poi)
sp (i.e., Px^1/sp ba) 40 ♀ extremely px and blist. like Px^1/ba
18 ♂ not poi, the same
13 ♂ poi, no periclinal or parallel veins, no or little antler or net

that is, svr^{poi} has the same action on balloon exaggeration as on bs. A remarkable fact is that here the pointed males show speck, which is otherwise suppressed by the pointed locus. The exaggeration effect of the deficiency prevents this phenotypic suppression.

Thus we see that the svr^{poi}, not containing bs, from which it is derived, has a developmental interaction of a suppressor type both with bs and ba, located near each other just as was the case with the near-by locus sp. $Svr^{poi\,h}$ not derived from bs has no interaction with bs, ba. I have no explanation to offer for this interrelation which does not appear fortuitous, as there is no experiment in favor of a bs duplication in the poi chromosome. We shall meet later with a small insertion into the first chromosome of poi and poi h near facet which could contain the bs and ba loci, though the origin is unknown. But actually two fewer bands are present in poi than in poi h, which makes this translocation not available for an explanation of the facts just noted.

Sex ratios and lethal classes.—It has been noted in the proper columns of tables already presented that F_1 and F_2 from pointed crosses showed abnormal sex ratios, which might mean a differential viability of flies with the pointed X chromosome or genetic lethal conditions. The analysis revealed a very complicated situation which somehow must be connected with the production of the mutant. It will simplify the description if we first assemble the main results and derive a hypothetical interpretation before we present the data. The following apparently contradictory facts are decisive:

a) Within the two pointed lines the sex ratio was always found normal.

b) The same is true for reciprocal crosses between svr^{poi} and $svr^{poi\,h}$, though the variation is larger than in the pure broods.

c) The number of flies in the offspring of a pointed pair is about ½ of that in the controls.

d) F_1 from wild type or marker ♀ and pointed ♂ have a normal sex ratio.

e) F_1 from an attached X ♀ with poi ♂ has a normal sex ratio.

f) The following F_1, F_2, and RF_2 contain, as a rule, male lethal classes in different ratios: poi × N ♂; (poi × N) × N, (N × poi) × N, $(N \times poi)^2$.

g) The backcrosses (poi × N) × poi, (N × poi) × poi, poi × (N × poi), poi × (poi × N) have, as a rule, a normal sex ratio.

h) The combinations with abnormal sex ratios seem to contain different ratios, both in F_2 and RF_2.

i) The standard translocation text y, bw, e ey × (ditto × poi) is negative.

k) A test with backcrossing (poi × bw e ey) × bw e ey shows poi ♂ missing in definite classes and ratios.

l) Backcrosses with marked second or third chromosomes reveal lethal combinations of poi with definite regions of these chromosomes.

These data exclude ordinary lethal loci in the pointed X chromosome. They exclude ordinary reciprocal translocations with lethal duplicated or deficient classes; they require a difference between the pointed X directly derived from a male (N × poi, y × poi) and such an X derived from a pointed female or a female heterozygous for pointed, whether the poi X is grandmaternal or grandpaternal. Thus they require nonreciprocal translocation from the poi X chromosome into autosomes, which produce male lethal deficiencies in the X of males and, in the proper crosses, in both sexes (which restores the normal sex ratio). Finally, the absence of lethal

TABLE 12

FREQUENCY OF BROODS

Cross	♀ : 1 ♂														
	0.6–0.8	–1.0	–1.2	–1.4	–1.6	–1.8	–2.0	–2.2	–2.4	–2.6	–2.8	–3.0	–3.2	–3.4	Many
$svr^{poi} \times N$	1	3	3	8	11	7	6	3	..	..	2	1	1	..	1
$svr^{poi\,h} \times N$	1	2	13	11	6	10	2	3	2	2	1	1	1	2	5[a]
$svr^{poi\,h} \times svr^{poi}$	..	2	1	1	2	1	..	..	..	..	..	..	..	..	..
$svr^{poi} \times svr^{poi\,h}$	1	1	3	2	2	..	..	..	..	..	..	..	..	..	..

Cross	N	Mean sex ratios	Mean number in brood
$svr^{poi} \times N$	5835	1.5	124
$svr^{poi\,h} \times N$	7822	1.5	126
$svr^{poi\,h} \times svr^{poi}$	952	1.3	136
$svr^{poi} \times svr^{poi\,h}$	985	1.2	109

[a] 309 ♀ 39 ♂.

classes in translocation tests with unbroken paternal poi chromosomes suggests the presence there of the translocated sections of the X chromosome from pointed as duplication, and this at a considerable distance from the deficiency to permit frequent crossing over. Thus the working hypothesis is: The X chromosome of pointed contains, in addition to the svr^{poi} mutant locus, (1) two nonreciprocal translocations from the X into the second and third chromosomes, respectively, (2) a simultaneous transposition of the same deficient loci into the regions to the right of the X chromosome, (3) variation and heterozygosity with respect to all these features within the stocks, and (4) parallel structure in both poi mutants.

We report now on the individual points (*a–k*, above).

a) Normal sex ratios within the pointed lines have been found again, to mention only the last check made for svr^{poi}, namely, 986 ♀ 895 ♂ = 1.1 : 1.

b) Tables 12–14 show the ratios and the frequency of broods (offspring of one pair) with the respective ratios in the reciprocal crosses of the two pointed mutants. There is a certain variation, with means ranging from 1 to 1.3. Table 12 shows at a glance that this variation is much smaller than in the other crosses, which, however, is not the case for the larger series in table 13 (made 3 years later). In both cases the crosses with $svr^{poi\,h}$ as mother have a higher sex ratio than the reciprocal crosses, indicating at least that the two strains are not completely alike.

TABLE 13*a*

SEX RATIOS IN DIFFERENT CROSSES WITH poi

Cross	♀ : 1 ♂									Total no. of flies	Avg. per bottle
	Frequency of broods								Avg.		
	Below 0.8	-1.0	-1.2	-1.4	-1.6	-1.8	-2.0	Above 2			
1. (Ore × svr$^{poi\,h}$) × Ore....	..	6	7	7	5	3	..	2	1.21	5456	181.8
2. (Ore × svr^{poi}) × Ore.....	..	4	13	7	5	..	1	..	1.18	5780	192.6
3. (svr$^{poi\,h}$ × Ore) × Ore....	..	4	10	9	4	..	2	1	1.22	5684	189.4
4. (svr^{poi} × Ore) × Ore.....	..	5	6	9	7	1	1	1	1.27	6173	205.7
5. Ore × (Ore × svr^{poi}).....	1	9	11	6	2	1	..	..	1.11	4608	153.6
6. Ore × (Ore × svr$^{poi\,h}$)....	..	7	12	3	3	3	1	1	1.15	4013	133.7
7. (Ore × svr$^{poi\,h}$) × svr$^{poi\,h}$.	1	3	18	2	3	2	1	..	1.16	5313	177.1
8. (Ore × svr^{poi}) × svr^{poi}...	..	7	14	5	1	1	1	1	1.14	5846	194.9
9. (svr$^{poi\,h}$ × Ore) × svr$^{poi\,h}$	1	2	19	7	1	..	..	..	1.12	5954	198.4
10. (svr^{poi} × Ore) × svr^{poi}...	..	7	12	9	2	..	..	..	1.11	5255	175.1
11. Ore × (svr^{poi} × Ore).....	1	13	14	..	1	1	..	..	1.01	5223	174.1
12. Ore × (svr$^{poi\,h}$ × Ore)....	2	5	17	4	1	1	..	..	1.09	5043	168.1
13. (svr$^{poi\,h}$ × svr^{poi})^2 F_2.....	2	8	16	3	..	..	..	1	1.06	4128	137.6
14. (svr^{poi} × svr$^{poi\,h}$)^2 F_2.....	..	6	11	7	4	..	1	1	1.19	4415	147.1
15. svr$^{poi\,h}$ × svr^{poi} F_1.....	..	4	8	5	6	3	1	2	1.28	2926	97.6
16. svr^{poi} × svr$^{poi\,h}$ F_1.....	1	11	9	5	2	1	..	1	1.05	3092	103.1

TABLE 13*b*

STATISTICAL TESTS OF TABLE 13*a*

Cross no.	Significance		Homogeneity		Broods differing significantly from 1 : 1	
	χ^2	P	χ^2	P	Number	Ratio
1	50.7	<0.01	71.7	<0.01	10	1.2–2.3
2	37.5	<0.01	48.0	<0.02	9	1.1–1.9
3	55.3	<0.01	61.5	<0.01	12	1.3–2.5
4	86.4	<0.01	71.2	<0.01	13	1.2–2.8
5	11.45	<0.01	38.99	>0.01	4	0.7–1.6
6	18.9	<0.01	44.7	<0.05	7	1.4–2.2
7	29.8	<0.01	41.8	>0.05	6	1.5–1.9
8	25.7	<0.01	44.3	<0.05	4	1.3–2.1
9	18.03	<0.01	17.43	>0.95	2	1.4
10	13.98	<0.01	27.42	>0.50	1	1.4
11	0.15	>0.50	28.71	>0.30	2	0.7–1.6
12	9.18	<0.01	38.04	>0.10	3	0.7–1.8
13	3.04	>0.05	24.56	>0.70	2	0.5–2.1
14	32.90	<0.01	43.93	<0.05	6	1.5–2.6
15	44.00	<0.01	43.86	<0.05	11	1.5–2.9
16	1.77	>0.10	33.90	>0.20	3	1.6–2.2

c) Table 12 does not give reliable information on the average number of flies in pointed broods, because the counts were made without this in mind and are therefore not comparable. But the data in table 13 were collected so that they are strictly comparable. Clearly, the average number of individuals in the outcrosses is almost twice that of the F_1 between the two pointed lines. F_2 of the pointed lines is, however, a little higher.

e) This is illustrated by a series of crosses, with the results shown in table 14.

f) Table 12 contains the sex ratios for a considerable number of pair crosses between females of the two pointed stocks and wild-type males, or such with different recessive markers. The variation of the sex ratios is a very considerable one. About half the broods show ratios above 1.5 : 1, an appreciable number even 2–3 : 1, and some broods contain hardly any males. The statistical analysis of the table has been made the following way. From the original data only broods with more than 50

TABLE 14

CROSSES $\underline{y} \times$ poi

Cross	♀	♂	Ratio
$\underline{y} \times svr^{poi}$	152	194	0.8
$\underline{y} \times svr^{poi\,h}$	252	311	0.8
$\underline{y} \times (\underline{y} \times svr^{poi})$	622	617	1.0
$\underline{y} \times (\underline{y} \times svr^{poi\,h})$	152	161	1.0

individuals were selected. There were 28 broods for svr^{poi} and 45 broods for $svr^{poi\,h}$. For each one χ^2 was calculated on the assumption of a 1 : 1 ratio. Those which differed significantly ($P < 0.01$) were successively tested for the expectations 4 : 3, 8 : 5, 2 : 1, and 4 : 1, as derived from the interpretation. All those which fitted any of these expectations were subjected groupwise to a homogeneity test. Thus almost 200 χ^2 were calculated, and 8 homogeneity tests. The results were:

svr^{poi}

Of 28 broods, more than 50 individuals:
- 14 fit a 1 : 1 ratio, and together they give a homogeneity of 9.15, $P > 0.70$
- 14 differ significantly from a 1 : 1 ratio ($P < 0.01$) when tested for the different expected ratios
- 11 fit a 4 : 3 ratio with a homogeneity 2.85 ($P > 0.98$)
- 13 fit an 8 : 5 ratio, homogeneity 7.56 ($P > 0.80$)
- 11 fit a 2 : 1 ratio, homogeneity 7.51 $P > 0.50$
- 1 fits a 4 : 1 ratio

$svr^{poi\,h}$

Of 45 broods, more than 50 individuals:
- 25 fit 1 : 1 ratio, homogeneity 17.22 $P > 0.80$
- 20 differ significantly; of these
- 17 fit 4 : 3 ratio, homogeneity 6.4 $P > 0.98$
- 20 fit 8 : 5 ratio, homogeneity 11.14 $P > 0.90$
- 17 fit 2 : 1 ratio, homogeneity 6.56 $P > 0.98$
- 1 fits 4 : 1 ratio

This indicates that the expected ratios, with considerable overlapping, are actually present, though it would be difficult to say how frequently the ratios 1.33, 1.6, and 2 : 1 are represented. The ratios have been derived from the assumption that two different nonreciprocal translocations from the first into the second and third chromosomes are present. The details will be discussed with the tests for individual chromosomes. In a general way we learn from this table that pointed females must frequently be heterozygous for an X chromosome that is male lethal under certain conditions which cannot be simple and which might also include balanced lethals in the extreme rates (with a little crossing over).

The backcross combinations are found in table 13, where nos. 1–6 and 11 and 12 are the combinations which do not produce pointed females, and nos. 7–10 those which segregate both pointed females and males; nos. 13–15 are controls in two generations of crosses between the pointed mutants. The series was made so as to be strictly comparable in every respect, and where the sex ratios are in favor of the females it is always the pointed male class which is deficient. Of each cross, 30 individual pair crosses were made, and the sex ratios were calculated and arranged in a frequency table with classes of 0.2. We see again a considerable variation from normal, even a slight preponderance of males, to very high ratios, though the extreme ratios recorded in table 12 for F_1 are missing. Again, the frequency distribution of the different ratios indicates that the major deviations are significant. The same statistical tests were applied as before, i.e., the χ^2 for the 480 individual broods were calculated and the homogeneity test applied. Table 13*a* contains the results. The number of broods significantly differing from a 1 : 1 ratio is small when the X chromosome of the males is not derived from poi, also small in most of the controls and in the cases where females homozygous for poi could be produced and therefore lethal female classes were expected. The actual number of these significant abberations from 1 : 1 is, in percentages of all broods of the respective group:

Not poi X chromosome in males.....13.3 per cent
Crosses with poi females segregating..13.3 per cent
F_2 controls .....13.3 per cent
F_1 controls .....23.3 per cent

But in the crosses in which proper conditions for male lethal classes were present the percentage is 36.7. The homogeneity test was significantly negative for this same group but positive for all others except one (no. 5), though the χ^2 for many of these latter groups showed $P < 0.01$. Further analysis is hardly possible since segregation and, in many instances, crossing over must obscure the results. But in a general way the results agree with the foregoing. They also show, incidentally, the already stated nonidentity of poi and poi h (see 13–18, table 13*a*).

If we add all the crosses in which the poi X chromosome has been introduced by the maternal grandmother, paternal grandmother, etc., we get the results shown in table 15. This table is not very illuminating; nevertheless it shows clearly that the maximum of broods with male lethal classes is obtained when the mother is heterozygous (first and third group), thus giving a chance for crossing over in the X chromosome; that relatively few broods with lethal ♂ are found when the mother is not heterozygous for poi; that the same is true where ♀ and ♂ poi can be produced, i.e., eventual lethal classes in both sexes. Whereas pointed alone has a normal sex ratio, the control crosses between the two pointed are significantly different

from the other crosses, thus showing that both of them differ more or less in regard to the presence of the lethal conditions. The ratios of this table have been calculated for two limiting values of the sex ratios, 1.2 (below 1.2 : above 1.2) and 1.4 (below 1.4 : above 1.4). The latter ones show the relations more clearly, as expected. The explanation for all these ratios will be derived below and will be summarized in table 44.

TABLE 15

poi X derived from	Ratio frequencies below 1.2 : above 1.2 below 1.4 : above 1.4
Maternal grandmother	25 : 35 = 0.7 43 : 17 = 2.5
Paternal grandmother	52 : 8 = 6.5 56 : 4 = 14.0
Maternal grandfather	30 : 30 = 1.0 44 : 16 = 2.8
Paternal grandfather	40 : 20 = 2.0 49 : 11 = 4.5
Both parents, i.e., ♀♂ poi	84 : 36 = 2.3 107 : 13 = 8.2
Control F_1 poi h × poi	12 : 17 = 0.7 17 : 12 = 1.4
Control F_1 poi × poi h	21 : 9 = 2.3 26 : 4 = 6.5
Control F_2 (poi h × poi)^2	26 : 4 = 6.5 29 : 1 = 29.0
Control F_2 (poi × poi h)^2	17 : 13 = 1.3 24 : 6 = 4.0

We refer again to table 5 (p. 304), which has already been discussed in relation to expressivity of the character of pointed wings. The summarized results below show a perfect regularity of the sex ratios for F_2 of both alleles : F_2 with only males pointed show the high average sex ratios 1.4 and 1.6 respectively, which illustrates again point *g* above.

h) The tables studied in the foregoing section indicate that the individual pointed flies are not alike in regard to their X chromosome, which might be normal or abnormal in different ways. A constitution as assumed would leave in the population different types, by segregation and crossing over, and therefore variation of type as observed is to be expected.

i) As not only the sex ratios but also the marker tests indicate the presence of minute translocations from the X chromosome into autosomes (no major ones are present; see salivaries, below), the standard translocation test ought to reveal them.

Actually it is completely negative. As this is an important point, some data may be given (table 16).

The table shows neither lethal nor sublethal classes. Though a Patterson stock was used which had been highly selected for an extreme and easily visible eyeless, the backcross introduced dominant modifiers which make ey overlap with plus, as the addition of the complementary classes with and without eyeless shows. (See below). Moreover, controls show that the viability of the segregants decreases with

TABLE 16

Patt × (Patt × poi and poi h)

Mutant	♀							
	Patt	bw e	bw ey	e ey	bw	e	ey	+
poi	48	57	41	43	62	59	47	63
poi h	14	15	12	17	24	20	14	36
	bw e ± ey		e ± ey		bw ± ey		+ ± ey	
poi	105		102		103		110	
poi h	29		37		36		50	
Mutant	♂							
	bw e ey	bw e	bw ey	e ey	bw	e	ey	+
poi	44	34	56	40	55	58	66	76
poi h	14	16	17	21	23	18	30	22
	bw e ± ey		e ± ey		bw ± ey		+ ± ey	
poi	78		98		111		142	
poi h	30		39		40		52	

χ^2 = poi ♀ 10.2 ♂ 24.9 P ♀ > 0.10 P ♂ < 0.01
poi h ♀ 22.8 ♂ 8.9 P ♀ < 0.01 P ♂ > 0.30
χ^2 second grouping: poi ♀ = 0.36 P = 0.95 poi ♂ = 20.04 P < 0.01
poi h ♀ = 6.05 P = 0.10 poi h ♂ = 6.09 P 0.10

the number of recessive alleles. (Controls with Oregon in table 105). Significant χ^2 values therefore may relate to such irregular features. But the numbers for poi with the correction for overlapping ey show a considerable difference in males and females which cannot be accounted for by these features alone (see χ^2) in spite of a 1:1 sex ratio. Either the viability of the classes is unusually influenced in the presence of the pointed X, or the absence of the second and third chromosomes, and, still more, second and third chromosome derived from the poi line in presence of an X from poi decreases the viability: this being the more probable explanation.

We have already mentioned the fact that lethal male classes are obtained whenever the X chromosome of sons is derived from a heterozygous mother (poi/+), and that this is the case whether this X is of grandmaternal or grandpaternal origin. This shows that lethal deficiencies in the X chromosome are compensated in the male and not (or not only) by an autosomal duplication, since y × poi crosses have

a normal sex ratio. But a heterozygous mother produces male lethal classes, and we must therefore assume that the compensation present in the male is absent or can be broken by crossing over. This points to a transposition of the same locus or

TABLE 17

(svr^{poi} × bw; e; ey) × bw; e; ey

♀							
bw e ey	bw e	bw ey	e ey	bw	e	ey	+
9	17	15	10	14	18	8	25
15	17	11	10	27	20	10	19
13	14	10	19	24	14	9	27
17	14	13	7	25	16	12	18
5	3	3	1	4	3	2	4
4	2	3	5	3	4	4	6
15	19	8	10	25	26	9	20
12	8	15	7	28	17	13	38
12	22	9	6	25	28	8	30
14	20	12	5	29	23	18	17
12	21	8	6	17	16	6	23
128	157	107	86	221	185	99	227

	♂ + : poi each class																♀ : ♂
	bw e ey		bw e		bw ey		e ey		bw		e		ey		+		
	17	3	5	5	5	10	2	1	9	2	16	3	4	3	4	5	1.38
	18	2	4	1	6	6	5	4	12	8	11	2	1	3	10	7	1.29
	9	5	5	0	10	8	4	2	5	2	4	1	5	8	16	4	1.36
	7	2	4	1	6	5	4	3	15	8	8	1	5	3	11	7	1.36
	3	2	1	..	3	2	3	1	2	4	3	1	..	2	6	1	0.75
	..	..	3	2	..	2	1	..	..	..	1	1	..	1	..	1	2.58
	14	3	3	..	7	4	7	1	15	5	11	3	6	6	19	7	1.19
	7	2	4	..	7	6	7	1	8	6	10	3	6	3	11	..	1.70
	8	2	12	..	5	8	6	2	15	3	15	..	8	5	5	3	1.21
	10	6	5	..	5	5	3	4	10	9	17	1	6	3	9	5	1.41
	8	2	8	..	4	4	4	2	12	6	12	1	5	5	6	5	1.42
	101	29	54	9	58	60	46	21	103	53	108	17	46	42	97	45	1.36
Σ.....	130		63		118		67		156		125		88		142		
Ratio + : poi.	3.5		6		0.9		2.1		2		6.3		1.1		2.1		

χ^2 ♀ = 142.53 $P < 0.01$

χ^2 ♂ = 75.28 $P < 0.01$

χ^2 sex ratio for 4 : 3 = 0.34; $P > 0.50$; Homogen. $P > 0.70$

loci within the poi X to a considerable distance away from the deficiency, in addition to translocation into an autosome. First information on this point ought to be derived from similar crosses involving marked autosomes but introducing the poi X via a female. This leads to point *k* of our enumeration.

k) Tables 17 and 18 contain the results of the backcrosses (svr^{poi} × bw, e, ey)

× bw, e, ey. (The controls with Oregon are found in table 105.) Table 17 shows first a considerable deviation from a 1 : 1, etc., expectation (see χ^2) in both sexes. Looking over the data, one realizes at once that different features are involved: first, the already encountered suppressor action for eyeless more extreme here than before; secondly, the abnormal sex ratio; thirdly, definite features with respect to the ratios of plus : poi males which deviate from the expected ratios (poi does not mean the phenotype pointed wings which is dependent upon enhancers, but actually all poi pale = svr^{poi} males).

TABLE 18

(Like table 17, but ey and not ey classes combined)

♀				♂ + : poi each class			
bw e ± ey	bw ± ey	e ± ey	+ ± ey	bw e ± ey	bw ± ey	e ± ey	+ ± ey
				22 8	14 12	18 4	8 8
				22 3	18 14	16 6	11 10
				14 5	15 10	8 3	21 12
				11 3	21 13	12 4	16 10
				4 2	5 6	6 2	6 3
				3 2	.. 2	2 1	.. 2
				17 3	22 9	18 4	25 13
				11 2	15 12	17 4	17 3
				20 2	20 11	21 2	13 8
				15 6	15 14	20 5	15 8
				16 2	16 10	16 3	11 10
285	328	271	326	155 38	161 113	154 38	143 87
		Σ.....		193	274	192	230
		Ratio + : poi.....		4.05	1.42	4.05	1.63

χ^2 ♀ = 8.29 P = 0.05
χ^2 ♂ = 20.32 P = 0.01
χ^2 not e classes for exp. 4 : 3 = ♀ 0.34 P > 0.50, ♂ 2.38 P > 0.10

The situation for eyeless suppression becomes clear when we compare the reciprocal classes with and without ey; e.g., bw, e, ey : bw, e, etc., and when we compare the added reciprocal classes with each other, which is done in table 18. The females show a simple result. The classes plus : ey, bw : bw, ey and e : e, ey all show a ratio of approximately 2 : 1, and the classes bw, e : bw, e, ey, a ratio of 1 : 1. This shows clearly that the second and third chromosomes of poi contain a suppressor action for eyeless with such an effect upon about ⅓ of the eyeless males. Correspondingly, when the not eyeless and eyeless groups are added (see table 18) almost normal ratios of the groups appear. Special tests were made to prove this interpretation. They will be reported later when a corresponding but more extreme action in a different allele will be reported.

But still the groups containing e/e are smaller than those with e/+ with perfectly regular numbers, in both groups, and a ratio of 1.17. This requires that a third chromosome from poi enhance the viability of the females whether a second one is present or not. We do not know what this action is, but as small translocations into the second and third chromosomes of poi will be demonstrated, these are suggested

as being responsible for the suppressor effect as well as the viability effect. In all classes the first chromosomes are either poi/+ or +/+, which might mean that the actions are confined to the unbalanced combinations with normal first chromosomes. We may add that recently Pontecorvo (1943) came to the conclusion that lowered viability in partial hybrids of two *Drosophila* species is based upon very small translocations.

In the males (tables 17, 18) the situation is complicated by the presence of male lethal classes in the pointed groups. If we look at only the ey suppression we can distinguish here between males with and without the poi X. In those without poi X no lethal classes are involved and actually the added ey and not ey groups contain equal numbers of individuals of about ½ of the female classes (see table 18, summation). The ey suppression in not poi ♂ is the same in the plus, bw, e classes as is found in females (ratio 2 not ey : 1 ey), pointing to the explanation given above. But there is a strange ratio observed in the bw, e, ey : bw, e classes, the latter being half the size of the former. As both added have the expected number, we see in the males without a poi X now the opposite of ey suppression, namely, a dominance effect of ey in about ⅓ of bw, e, ey/+ ♂. As this result was not obtained in females (with actually more bw, e ♀ than bw, e, ey ♀), the X chromosome must be involved via crossing over, i.e., in the presence of an X without the poi end, but in the presence of other parts from poi to the right of this locus the dominance effect upon ey occurs even with second and third chromosomes not derived from poi stock. If this is the case, the responsible locus in the poi X would be located 30 units to the right of poi. One would like to think of a Dubinin effect involving a translocation 4→1. But as this does not tally with the ey suppression effect which is present in both females and males only in the presence of a second or third chromosome from poi, it seems more probable that no translocation 4→1 is involved, but a specific dominance-enhancing effect of a point in the X chromosome. If our assumption is correct that the suppressor effect is due to the duplications by translocation 1→2 and 1→3, this might mean that the same duplication in the form of a transposition acts as a dominance enhancer. This might be checked by a comparison with the Patterson crosses (table 16) in which the females have always non-poi X chromosomes but the same autosomes as in the present case, whereas all the males have a poi X chromosome without possibility of crossing over. Actually, the eyeless suppression is here rather small in both sexes though larger in the females, and the female classes added from eyeless and not eyeless show a perfect 1 : 1 : 1 : 1 ratio, whereas the males have very poor ratios. These data thus agree only in part with the conclusions just derived. Again, we shall return later to the same problem in connection with another poi allele which shows the dominance effect in extreme form.

We turn now to the more important problem, the distribution of male defective classes, which, as we saw, are limited to the group with the X chromosome containing poi, though such classes are always absent in the $\underline{y} \times$ poi crosses with all males possessing a poi X. We see from table 17 that the entire sex ratio is near 4 : 3 (1.36), and as we know that the not poi males are all present, ½ of the poi males are missing. But these are not equally distributed among all the autosomal classes, as the lower end of both tables shows. Actually the ratios are, if the correction for ey suppression is made (table 18), near 4:1 in both classes containing e/e, and near 1.5 : 1 in both classes with e/+, whether either is bw/bw or bw/+. When the correction for ey sup-

pression is not made (table 17), the ratios for e/e and bw/bw, e/e are near 6 : 1, those for e/e, ey/ey with bw/bw or bw/+, near 3 : 1; those for e/+ ey/+ with bw/bw or bw/+, 2 : 1; and those for ey with bw/bw or bw/+, 1 : 1.

The individual broods recorded in table 18 show that the high ratio of poi lethality is consistently present in all individual broods and therefore requires a single causation. As the majority (¾) of poi males in these groups are lethal, it is obvious that the poi X in the absence of proper third chromosomes (e/e class) is lethal except in) ¼ of the individuals, a fact which must be due to crossing over, as the other autosomes do not influence the result (taking into account the ey suppression). As the numbers of the not poi classes are exactly those expected from the female numbers (i.e., ½), the crossing over cannot have occurred in the X chromosome, since otherwise the same number of lethals would occur in the not poi class as there are survivors in the poi class. Therefore crossing over in the third chromosome between the locus of e and the locus of a nonreciprocal translocation 1→3 would account for the facts. If this is the case, equal numbers of crossover gametes containing e and the T and $+^e$ without T are formed. The latter are found in the backcross classes e/+, where, therefore, the same percentage of poi males must be missing as survive in the e/e classes. Actually, 25.4 per cent survive in the e classes (which would be the crossover value e–T) and 34.2 per cent are missing in the e/+ classes. This is roughly according to expectation, χ^2 of the not e classes for an expectation of 4 + : 3 poi is not aberrant, and the homogeneity test for all classes is positive. In spite of this, a comparison of the individual broods for the e/e classes shows very little variation, whereas the e/+ classes seem to contain two major types, one nearer 1 : 1, the other nearer 2 : 1. Thus probably there is involved in the ratios something else, which is not clearly visible here but seems to result from the fact that the individual broods are not alike. This means that different F_1 combinations exist, which again requires that the original poi female be heterozygous for something in one of the chromosomes. The details of an analysis of individual chromosomes now to be presented will point out such possibilities.

Tests for individual chromosomes: the second chromosome.—The following crosses are made with second chromosomes marked with ll sp. In the presence of homozygous or hemizygous pointed, speck is suppressed (completely in males, sometimes incompletely in females.) The ll (sp) class therefore is ll sp + poi (crossing over being only a fraction of 1 per cent. In F_2 both ♀♀ and ♂♂ of this combination are expected, and in the backcross only males. Table 19 shows a rather normal segregation for +, poi, and ll sp (7–8 not ll sp : 1 ll sp in F_2, 2 not ll sp : 1 ll sp in RF_2), but only a small number of ll=ll sp+poi. Either this class is semilethal, or it is completely lethal except for the crossovers between pointed and a lethal deficiency by translocation in the X chromosome (translocated into the second chromosome) and the crossovers between ll and the duplication in the second. If we call q_2 the crossover value between ll and the duplication in the second chromosome, and q_1 the crossover value between svr^{poi} and the deficiency in the first, the expected F_2 ratios for the males are:

$$300 + : 300 - \frac{q_2}{2} \text{ poi} : 100 - \frac{q_1}{2} \text{ ll sp} : \frac{q_1 + q_2}{2} \text{ ll (sp) poi}$$

This assumes that everything is normal except the translocation in question. Among the crosses reported in table 19 the second one clearly represents this situation,

since we have a normal sex ratio in the three large classes. The numbers of + and poi classes are not equal; the reason is that the classification had been made for the wing character alone, which is modifiable as reported above. In the last two broods the classification is a perfect one, in no. 4 by marking the tip of the poi chromosome with w, in no. 5 by checking for the pale color; and the two classes are equal. The ratio of + (and poi) : ll sp not poi ought to be near 6 : 1. It is actually much higher in most of the crosses; this indicates a lower viability of the segregating ll sp class or a further complication. The class of ll (sp) poi contains only a few males but more females. An exact calculation of $\frac{q_1 + q_2}{2}$ is prevented by the imperfect ratios for ll sp, but an estimate based upon the formula given above and the numbers for cross 2 would give a value for $q_1 + q_2$ of about 8 per cent for the males, i.e., both points would be rather near the markers. For the first chromosome we have the additional

TABLE 19

Cross	Broods	+		poi		ll sp		ll poi		Sex ratio
		♀	♂	♀	♂	♀	♂	♀	♂	
1. F_2 ($svr^{poi} \times$ ll sp)^2.....	8	586	586	216	51	103	44	26	2	1.36
2. F_2 ($svr^{poi\,h} \times$ ll sp)^2.....	9	678	675	201	191	117	101	21	6	1.04
3. RF_2 ($svr^{poi} \times$ ll sp) $\times$ ll sp...	2	179			187	133	81	...	2	1.15
4. F_2 ($svr^{poi\,h}$ w $\times$ ll sp)^2.....	1	26	30	26	26	3	3	3	5	0.9
5. F_2 ($svr^{poi} \times$ ll sp)^2.....	1	17	17	17	18	9	2	4	..	1.28

information furnished by cross no. 4. Here only the tip of the X chromosome from poi containing svr^{poi} is present, the rest being replaced to a point between w and svr. The two ll sp classes are equal, showing the deficiency to be located beyond the break between svr and w. A surprising fact is that a much larger number of ll poi females are recorded than males. It turned out (testing with ll sp) that they were actually mostly ll sp/+; poi/poi, ♀ with an unusually high grade of pointed which cannot be distinguished from a lower-grade ll; thus only the male numbers are reliable.

Backcross no. 3 is in agreement (expectation ♀♀, + : ll sp = 1 : 1, ♂♂, + and poi : ll sp : ll sp poi = 2 : 1 : c.o.). In the first F_2 some additional feature is present. One-fourth of the males are missing. If we assume that the plus class contains also a part of the pointed class with inhibition of the pointed character (see above), we expect 401 females 401 males +, 401 females poi; thus we actually have 236 males, poi, i.e., 41 per cent of the males are missing. In ll sp without poi more than ½ of the males are missing. If we assume that the translocation from X to the third chromosome found before was present in these crosses (together with that for the second chromosome), and if the locus of the deficiency in the first chromosome is near svr, we expect ¼ of the poi males to be missing. But in ll sp without poi only the crossovers in the first chromosome between svr and the deficiency would be missing among ¼ of the class. Thus something else affecting the males must be present. If there were a transposition in the X in addition to the two deficiencies, and the deficient point were far away from svr but the transposed section nearer it, a small

percentage of lethal male combinations would be added to the poi class (double crossover with poi and the far-away deficiency), and a larger number of not poi males would be lethal by crossing over between insertion and deficiency. The data hardly permit a decision except that the number of 11 sp males is still too low for such an assumption.[4]

TABLE 20

$(svr^{poi} \times a) \times a$

No.	♀		♂			a poi
	+	a[a]	+	poi	a	
7979 B	99	72	45	27	54	1
7982 B	62	45	11	4	22	1
7983 B	80	82	36	14	34[b]	..
7985 B	88	95[c]	36	33[d]	63	1
7986 B	88	65	43	8	27	3
7988 B	81	67	43	26	37	..
Sa	498	426	214	112	237	6(?)
	♀+	♀a	♂+	♂ poi	♂ a	♂ a poi
Expected	462	462	231	231	231	231
Found	498	426	214	112	237	6

[a] a = arc.
[b] 5 ♂ spoon-like blist wings.
[c] 1 ♀ a blist.
[d] 1 ♂ blist.

TABLE 21

Cross	+	♂		a poi
		poi	a	
$(svr^{poi\,h} \times a) \times a$	176	81	177	9 (?)
$(svr^{poi} \times a) \times a$	186	82	182	15 (?)

We continue with the second chromosome. Table 20 contains a set of crosses $(svr^{poi} \times a) \times a$ which were made in 1935 soon after svr^{poi} had appeared. Table 21 contains a repetition, made six years later for both pointed alleles, giving only the sum total of the males. It is obvious that the ratio of 8 ♀♀ : 5 ♂♂ = 1.6 found in both cases is based upon the absence of ½ of the pointed males and of almost all of the arc pointed males. (The females are as expected.) The arc locus (or region) of the poi stock is therefore needed if the poi X is present in males, which again points to the nonreciprocal translocation from the poi chromosome to the right end of the second. In addition, another condition makes ½ of the poi males disappear, which is clearly the already studied translocation 1→3. (Actually a, poi [a pale or a px (sp) pale] can be isolated and bred if a pointed stock without the translocation is used.) Again, a small number of a, poi males survive marked with (?). The reason is the already

[4] It was found later that the ll sp stock contained a homozygous lethal inversion in the third chromosome. But this cannot be involved in the aberrant results, since it affects all segregating classes.

known weak dominance effect of arc in crosses with pointed. Therefore the number of arc poi males might also contain some of these heterozygotes. This makes an exact calculation of the crossover value impossible. At best it must be very low (see the formula given above). Probably the locus of the translocation is very near arc, and the few survivors are the crossovers in the first chromosome.

TABLE 22

(svr^{poi} w × a px sp) × a px sp

(Only ♂; px sp neglected, but a poi checked by sp suppression)

Sa.	a	+	svr^{poi} w	a svr^{poi} w
1	13	14	17	11
2	11	14	9	12
3	18	10	10	9
4	15	23	19	17
Sa. 1–4	57	61	55	49
5	24	19	9	6
6	22	19	15	8
7	17	27	10	9
Sa. 5–7	63	65	34	23

A first check upon this result is, as in the case of ll sp, the use of a pointed in which the part to the right of the X chromosome including white has been replaced by crossing over, i.e., the combination svr^{poi}w. If the deficiency by translocation is located to the right of white the lethality with a/a ought to be absent. Table 22 (only males registered) contains the answer. It is obvious that the almost complete lethality of a/a, poi males is here absent. Two groups of ratios are visible. The first (1–4) is practically normal. In the second (5–7), ½ of the pointed males are miss-

TABLE 23

(a px sp × svr^{poi}) × a px sp

+	♀					♂			C.o. and poi sp	Sex ratio
	a px sp	a	a px	sp	+	a px sp	poi	a px		
248	207	1	6	18	108	92	61	22	1	1.7

ing in both classes, a result which we saw before as being independent of the second-chromosome translocation, actually based upon the translocation 1→3 reported above. It turned out in this and many other crosses that pointed individuals from stock might contain one or the other, or both, or none, of these translocations.

Other checks were made, involving markers in the right end of the second chromosome, which permit a check on crossing over. In one of these the pointed X was introduced via a pointed male; the result is summarized in table 23, which again shows the sex ratio 1.7 based upon both translocations 1→2 and 1→3. The female crossover classes are about the expected ones (distance a–px 1.3, px–sp 6.5). In the

males crossovers a px with or without poi and a px sp, poi with sp suppression were not clearly distinguished. But if we estimate the crossovers from the normal expectation (not forgetting the lethal classes), only a small proportion of apx (sp) poi males remain, as in the other examples. In view of this similarity the translocation ought to be to the left of arc. Two other sets using the markers a sp and px bw sp gave essentially the same results, though a higher crossover value, i.e., survival of more pointed males with foreign second chromosomes was found. This point will be discussed below (see table 28). Also, reciprocal F_2 were used, in one of which lethal female classes are expected. The segregation again showed the same phenomenon and also a higher crossover value for the X chromosome, namely, about 10–12 per cent. But admittedly the calculations are not very reliable.

Only one more test, with quintuple = b pr vg a sp, will be mentioned, because it was made immediately after the appearance of pointed (table 24). It shows that at that time the translocation 1→3 was not present in the tested individuals, but the translocation 1→2 was there (sex ratio 1.36). It must be kept in mind that poi suppresses sp and that the flies containing vg which do not show the pointed wing character had not been checked for pale color. Flies with arc may be arc or a (sp) with poi. According to expectation, plus males are ½ poi, and among the quintuple flies nearly ½ with poi are missing. (A part of the 5 ple not poi males will be crossovers poi→Df.) The crossover classes with b and pr contain ½ pointed flies. The classes containing arc have only ½ of the males, the pointed males being lethal. The class arc alone gives information upon the surviving a poi males. Crossover males ought to equal the females in number; the rest are survivors a sp and poi. As there are 123 a sp females, about 60 males a sp poi are expected. Twenty survivors, i.e, about 33 per cent, is an unusually high percentage. The class b pr vg (a), in which arc cannot be distinguished, contains 140 females, 107 males, the missing males being those containing arc and poi. The number agrees with the expectation if the translocation is between vg and a near the latter (vg–a = 22.2).

One of the broods in table 24 is very strange and aberrant, namely, no. 6474. Here all plus males are poi, which requires a condition in an autosome, lethal if poi is not present (in addition to the known translocation). In b pr vg (a) most males are missing, and all males, not only those with poi, in the a sp and sp classes. The latter would be the combination of the plus lethal with the poi lethal condition. The result is a very high sex ratio, 146 : 62 = 2.3). The numbers of the a sp class seem to put the disturbance in the second chromosome between vg and a. The situation never recurred so as to permit of an analysis.

We reported that in later tests svr^{poi} and $svr^{poi\,h}$ gave the same results for the second chromosome and frequently also those expected for the 1→3 translocation, or both. Soon after the appearance of poi (1935), $svr^{poi\,h}$ was tested in the same way (nos. 7737–43, 7746–51 B). Among 10 backcrosses with the markers a sp and px bw sp, 8 contained the translocation from the first to the second chromosome (a px region) with the consecutive sex ratios, e.g., classes a sp and px bw sp.: 283 ♀ 125 ♂. In addition, there were 46♂ px bw (sp) and a (sp) and 11 such females, i.e., in 35 males with pointed in two broods the translocation was absent as far as these data go, or at least not present with certainty. There was no clear indication of an otherwise lethal poi class (though it was found in other similar crosses), which then, it seems, was only selected out later in this stock (see below: the third chro-

TABLE 24

(svr^{poi} × 5 ple) × 5 ple

Class	6032			7754			7458			7455			7456			7451			7459			7460			6474			6476			Σ		
	♀	♂	♂ poi	♀	♂	♂ p	♀	♂	♂ p	♀	♂	♂ p	♀	♂	♂ p	♀	♂	♂ p	♀	♂	♂ p	♀	♂	♂ p	♀	♂	♂ p	♀	♂	♂ p	♀	♂	♂ poi
+	28	10	17	27	18	6	27	9	8	17	13	12	13	6	8	33	14	15	25	12	16	34	14	9	44	..	32	37	18	17	295	114	140
5 ple	20	20	..	25	11	..	20	15	..	22	9	..	5	8	..	25	19	..	29	23	..	28	18	..	39	10	..	24	12	..	237	145	..
b	1	..	..	..	2	..	..	1	..	..	..	..	..	..	1	2	2	..	..	..	..	..	..	..	..	..	2	1	3	1	4	8	4
pr vg (a) sp	4	1	..	..	1	..	..	1	..	..	..	..	..	..	..	..	..	..	2	..	..	..	..	..	2	1	..	1	..	..	9	4	..
b pr	3	1	3	3	1	..	3	2	1	1	1	1	1	2	..	1	..	..	2	..	..	1	1	..	2	..	1	4	1	..	21	9	6
vg (a) sp	9	2	..	3	2	..	3	3	..	2	1	..	..	1	..	2	..	..	2	1	..	2	1	..	2	3	..	5	..	..	30	14	..
b pr vg (a)	20	20	..	7	5	..	17	10	..	9	9	..	4	3	..	14	10	..	14	20	..	10	7	..	29	5	..	16	18	..	140	107	..
a sp	14	11	..	7	6	..	9	4	..	11	1	..	8	4	..	14	9	..	12	3	..	12	7	..	20	..	..	16	7	..	123	52	..
sp	6	2	..	2	..	..	1	4	..	4	..	..	1	..	..	6	..	..	2	..	..	2	2	..	2	..	..	3	2	..	29	10	..
b vg (a) sp	..	1	..	..	2	..	1	..	..	..	..	..	1	..	..	..	1	..	..	..	..	..	..	..	..	..	..	..	..	..	2	4	..
b pr a sp	1	1	..	..	1	..	..	..	..	1	..	..	1	1	..	1	1	..	1	2	..	..	..	..	1	1	..	..	..	..	6	7	..
vg (a)	..	3	..	1	1	..	1	..	..	..	..	..	..	2	..	2	..	..	..	1	..	1	3	..	3	..	..	2	1	..	10	11	..
a	..	7	..	2	2	..	3	..	..	..	..	..	..	..	..	..	3	..	..	5	..	..	1	..	..	5	..	1	..	3	6	26	..
b pr sp	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	1	..	..	1	..	..
b a sp	1	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	1	..	..
pr vg (a)	..	1	..	..	1	..	..	..	..	..	..	..	..	..	..	..	..	..	1	..	..	..	..	..	1	2	..	1	..	..	2	5	..
b pr a	3	1	..	2	..	..	1	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	6	1	..
b vg (a)	..	1	..	..	5	..	..	1	..	..	..	..	..	1	..	..	4	..	..	..	..	..	..	..	1	..	..	..	..	..	1	12	..
pr	..	..	..	..	..	..	1	..	..	..	..	..	..	..	..	1	..	..	..	..	..	..	3	..	..	..	..	..	..	..	2	3	..
	110	82	20	79	58	6	87	50	9	67	34	13	34	38	9	102	63	15	90	57	16	90	57	9	146	27	35	112	62	21	925	529	153

Sex ratio = 1.36.

TABLE 25

(poi × triple) × triple

Class	SVR^{poi}			SVR$^{poi\ h}$			Sex ratio		♂ + : 1 ♂ poi	
	♀	♂		♀	♂		SVR^{poi}	SVR$^{poi\ h}$	SVR^{poi}	SVR$^{poi\ h}$
		+	poi		+	poi				
+	62	27	20	82	33	17	1.32	1.64	1.35	1.94
ru h st p^{p} ss e^{s}	34	22	6	48	35	1	1.21	1.33	3.67	35.0
ru	18	8	7	24	13	14	1.20	0.9	1.14	0.93
h st p ss e	29	7	2	21	9	..	3.22	2.33	3.5	∞
ru h	17	9	3	23	19	6	1.42	0.9	3.0	3.16
st p ss e	17	6	3	27	11	1	1.89	2.25	2.0	11.0
ru h st	2	..	..	..	3	1				
p ss e	3	..	..	2	..	..				
ru h st p	3	4	..	7	1	1				
ss e	6	2	..	5	5	..				
ru h st p ss	11	5	2	8	9	1	1.43	0.8	2.5	9.0
e	13	8	4	17	10	..	1.08	1.7	2.0	∞
ru st p ss e	5	..	..	1	..	..				
h	5	..	..	3	4	1				
ru h p ss e	1	..	..	..	..	..				
st	1	1	..	1	..	1				
ru h st ss e	1	..	..	..	..	..				
ss	1	..	..	..	..	..				
ru h ss e	2	3	..	..	2	..				
st p	2	2	1	2	..	..				
ru p ss e	..	..	..	1	1	..				
h st	..	..	..	1	1	..				
p ss	2	..	..	3	..	..				
ru ss e	2	4	2	3	1	..				
h st p	2	1	2	2	1	2				
ru h e	3	2	1	3	..	..				
st p ss	6	3	2	4	3	1				
ru e	2	4	..	5	..	..				
h st p ss	1	2	..	7	5	..				
h ss e	..	1	..	..	..	..				
ru st p ss	..	2	..	1	..	..				
h e	..	..	1	3	1	..				
ru h st ss	1	..	..	..	..	..				
h st e	..	1	..	..	..	..				
ru ss	..	1	..	..	..	..				
h p ss e	..	..	..	1	..	..				

mosome). Other localization tests made with other pointed alleles all agreed with a localization of the translocation near and to the left of arc.

We remember that F_1 poi × arc always showed a slight dominance effect of arc not observed otherwise. If the translocation into the second chromosome is actually located next to arc, as the salivaries indicate (see below), the arc segment might be involved and the compound effect a/T might actually be a position effect in this segment. We further reported above the presence of a dominant enhancer for pointed wings in this stock, and that we found a better expression of pointed wings

in males from the cross poi × N when N contained arc. There is a possibility that this enhancer is identical with the translocation, but an exact test would be very difficult to perform and was not tried.

Tests for individual chromosomes: the third chromosome.—We found in the analysis of the second chromosome that in addition to the translocation X→2 near arc, which produced deficient male lethal classes, another condition was present in

TABLE 26

CROSSING OVER TABLE 25

C.o.	♀	♂	Standard
ru–h	24.9	24.0	26.5
h–st	22.0	22.2	17.5
st–p^p	3.2	2.6	3.5
p^p–ss	6.8	9.0	10.5
ss–e^s	16.4	16.2	12.2

some of the crosses which eliminated also ½ of the normal males. A similar translocation into the third chromosome from the first was assumed on the basis of former data (the bw, e, ey crosses) which had demonstrated such a nonreciprocal translocation. Those earlier data permitted a rough estimate of the localization which will now be tested with marked third chromosomes. Table 25 contains the summarized results for three backcrosses of svr^{poi} and $svr^{poi\ h}$ × triple (ru h st p^p ss e^s), all made soon after the appearance of svr^{poi}. Crossing-over values are rather high in some

TABLE 27

RATIOS FOUND IN THE TRIPLE BACKCROSS, TABLE 25

	svr^{poi}			$svr^{poi\ h}$			Sex ratio		♂ + : 1 ♂ poi	
	♀	♂ +	♂ poi	♀	♂ +	♂ poi	poi	poi h	poi	poi h
All small classes with e...	25	17	4	24	10	..	1.24	2.4	4.25	∞
All small classes without e	26	16	5	31	18	7	1.24	1.24	3.20	2.57
All classes with e.....	118	60	19	137	75	2	1.49	1.78	3.16	37.5
All classes without e.....	134	65	37	168	92	55	1.31	1.15	1.76	1.67
All classes ru, not h, not e.	18	11	7	24	13	14	1.0	0.9	1.57	0.93
All classes h, not ru, not e.	8	3	2	13	11	3	1.6	0.9	1.50	3.66
All classes ru h, not e.....	34	18	5	38	32	9	1.48	0.97	3.6	3.56

classes (see table 26), though not much significance is attached to this (aside from corrections for lethal classes).

There is a considerable difference between the two groups of crosses. In all crosses with $svr^{poi\ h}$ there is a clear difference between reciprocal crossover classes: all not containing ebony have an approximately normal sex ratio, those with ebony have a high sex ratio (for this and the following see the ratios at the right side of table 25 and the summarized ratios in table 27). The ratios of plus : poi h males are extremely high in the presence of ebony; actually there is practical lethality of e, poi h males. As nearly all classes with e from triple to e alone are almost devoid of poi h males, whereas the proper number of plus males are present, the insertion is probably

located to the right of e (70.7). A little information is given by the double (and more) crossover classes without e, which will often contain the insertion except when there is another crossover break between e and the insertion. Actually these classes (table 27) contain poi h males, but less than half the expected number, which roughly agrees with a localization far to the right of e. The few e, poi h males indicate that the deficiency in the first chromosome is located very near the pointed locus, the few poi males being the crossovers between poi→Df. In the not ebony classes the + : poi h male ratio is normal in some crossover classes, high in others. This latter fact, however, has a different significance. We remember (see p. 304, above) that a dominant modifier for the expression of the pointed character (wing) is located in the third chromosome. Thus, whenever there is a normal sex ratio but too few pointed phenotypes it has to be assumed that this phenotypical modification is involved wherever the classification was made for the wing character, which was the case in the earlier work. In all these classes with normal sex ratio (not e) about ½ of the males are visibly pointed when ru is present but not h, whereas in the classes h, not e, not ru a normal sex ratio combines with almost ⅘ of the males not poi. The same is true for classes ru h not e. The enhancer is thus localized between ru and h at the left end of the third chromosome (see table 27).

In the noncrossover classes, especially the triple class, the numbers are less good. A comparison with the plus class shows that the triple females are less viable, which makes for a too low sex ratio. If this were corrected, the class would agree with the other results. In the plus class as well as in the crossover classes the ratio + : poi ♂♂ is nearer 2 : 1 with a sex ratio near 4 : 3, which is expected if the second-chromosome translocation is simultaneously present.

In this set, made shortly after the appearance of svr^{poi}, this allele gave different results from those obtained for $svr^{poi\ h}$. The summarized data are rather irregular. The individual data seem to indicate that one backcross behaved like $svr^{poi\ h}$ and that the others lacked the third chromosome translocation, which together makes for a result between the one discussed and normalcy. But the individual numbers are too small for a reliable statement. Tests made later with the svr^{poi} stock revealed that the third-chromosome translocation was frequently absent (see below for other alleles), but that the intensifier was present, which latter again turned out to be located between ru and h. All crossover classes with the right end of the third chromosome derived from the marker stock contain 99 + : 33 poi; the reciprocal classes with the right end from poi third chromosome 49 + : 50 poi. As the classes with fewer poi males are even larger than the equal ones no lethal class is involved. Altogether the results reported for the second and third chromosome indicate that the 1→3 translocation is sometimes present and sometimes not. It seems that originally it was more frequent in $svr^{poi\ h}$, but this might have been purely accidental, depending upon the individuals selected for breeding from a mixed stock.

Years later, the end of the third chromosome beyond ebony was tested again for the translocation with the markers st sr e^s ro ca (e^s ebony 70.7 ro rough 91.1 ca claret 100.7). In all crossover classes there were as many pointed as not pointed males, with the exception of the class st sr e^s ro (the reciprocal class ca being normal), in which there were almost no poi males, the number being statistically significant. This puts the translocation between rough and claret in agreement with former data.

Some additional data for the second and third chromosomes.—The data on the second chromosome showed that in different tests made at different times two types of result appeared (see p. 323). In one group the combination of homozygous foreign second chromosomes with the pointed X was practically lethal except for a few survivors by crossing over. But in the original records these crossover individuals showing arc had received an interrogation mark, and, as the F_3 tests showed, certainly some of them were not reliably classified (in this case because of the heterozygous arc effect). Thus the insertion is supposed to be practically at the arc locus and the deficiency rather near the svr locus. In another set of experiments a much higher rate of survival was found, with rather consistent values. Table 28 summarizes these values (part of them taken from preceding tables).

TABLE 28

FURTHER CROSSES poi × SECOND-CHROMOSOME MARKERS

Cross	♂ marker not poi	♂ marker and poi		Percentage of survivors
		absolute	corrected[a]	
(a px sp × svr^{poi}) × a px sp	92	22	16	17.4
(5 ple × svr^{poi}) × 5 ple	52	26	20	38.4
(a sp and px bw sp × svr^{poi}) × a sp	78	30	22	28.2
(px bw sp × svr^{poi}) × px bw sp	115	49	45	39.1
(a px sp × svr^{poi})^2	24	7	7	29.2
(svr^{poi} × a px sp)^2	59	21	12	20.3
Sa	420		122	29

[a] The correction consists in subtracting second-chromosome crossovers of the same phenotype found also in the ♀ and thus expected to be contained also among the poi ♂.

These facts (those reported above and those considered here) suggest the hypothesis that in some pointed individuals only the translocation 1→2 is present, with the deficiency in the first chromosome near the svr locus; and that in other individuals a duplication for the same region is present somewhere else, which might be a second translocation of the same section near poi into the third or a transposition within the X chromosome. We shall see when studying the first chromosome that the facts agree with the latter assumption. In the presence of the additional 1→3 translocation one-half of the combinations with pointed is expected to be missing even if the deficiency by translocation 1→2 is compensated by a duplication. If a transposition within the X chromosome is responsible for this duplication, the noncrossovers between the deficiency and the transposition will be the survivors, but again half will be lethal because of the 1→3 translocation. Thus a crossover value within the transposition of about 20 per cent would be derived from table 28. We shall find the possible locus somewhere near 33 in the first chromosome.

But there are some difficulties in this explanation. It is true that pointed males with the foreign second chromosome were almost completely absent in a series of crosses in which a female had introduced the poi X. Such a female may be heterozygous for two types of X. In the crosses tabulated in table 28, however, the poi X was introduced in all but one via a male, which must have had compensation for the

deficiencies, as the translocation tests and the crosses with y had shown. This is in agreement with the transposition hopothesis. But here is a difficulty: the first set showed clearly another lethal condition (½ males poi in the plus class missing), which we assumed to be the translocation 1→3. This again requires for the normal males used in the translocation and the y tests a duplication for this translocation, as no males were missing and no compensating female lethal class could be expected. The present data (not contained in table 28) show that no pointed plus males are missing. This must mean that in this set the third-chromosome translocation was absent, and therefore no conclusion upon an eventual transposition for this translo-

TABLE 29

EXPECTED RATIOS

Autosomes of F_1 mother		X chromosome of RF_2 sons	Sex ratio, c.o. class with DF	Sex ratio, reciprocal c.o. classes, one with DF
2d	3d			
Normal	Normal	DF tr.→2	1 : 0	2 : 1 = 2
Normal	Normal	DF tr.→3	1 : 0	2 : 1 = 2
Normal	Normal	Both DF	1 : 0	2 : 1 = 2
Heterozygous insertion	Normal	DF tr.→2	2 : 1	4 : 3 = 1.33
Heterozygous insertion	Normal	DF tr.→3	1 : 0	2 : 1 = 2
Heterozygous insertion	Normal	Both DF	4 : 1	8 : 5 = 1.6
Normal	Heterozygous insertion	DF tr.→2	1 : 0	2 : 1 = 2
Normal	Heterozygous insertion	DF tr.→3	2 : 1	4 : 3 = 1.33
Normal	Heterozygous insertion	Both DF	4 : 1	8 : 5 = 1.6
Heterozygous insertion	Heterozygous insertion	DF tr.→2	2 : 1	4 : 3 = 1.33
Heterozygous insertion	Heterozygous insertion	DF tr.→3	2 : 1	4 : 3 = 1.33
Heterozygous insertion	Heterozygous insertion	Both DF	4 : 1	8 : 5 = 1.6

DF = deficiency; tr. → = translocated into.

cation could be drawn in these experiments. We shall return to this problem when discussing the first chromosome.

Tests for individual chromosomes: the first chromosome.—The complicated expectations for the first chromosome are contained in the foregoing discussion. The decisive points of that analysis are: (1) A very small section of the X chromosome has been translocated into the right end of the third chromosome. The resulting deficiency is expected to be rather closely linked with svr^{poi}. (2) Another small section of the X chromosome has been translocated into the second chromosome in the arc region. The crossover values indicated again a position in the X chromosome near svr^{poi}. (3) The fact that translocation tests were negative when unbroken X chromosomes (no crossing over) were involved requires not only that the deficient portions of the X be translocated into the second and third chromosomes, but also that they be transposed into the right part of the X itself. No other interpretation of all the facts seems possible, as the participation of the Y chromosome can be ruled out (normal sex ratios in F_1 and F_2 of $\widehat{XXY} \times$ poi). The probable locus of the transposition of the piece otherwise translocated into the second chromosome was about 20 units from svr. (4) The individuals of the pointed stocks did not all appear alike. It seems that the deficiencies in the first chromosome were not always present; actually that either, both, or none of the translocations might be found in

TABLE 30

$(X^4 \times svr^{poi}) \times X^4$

Class	Number/broods																						Total		Total
	152/3		131/2		128/2		T 7/2		126/1		125/1		T 1/1		T 2/1		T 3/1		T 8/1		T 9/1		♀	♂	
ct⁶ v wy² f	77	81	83	53	101	70	62	39	31	26	32	26	44	21	17	6	33	23	21	18	0	2	501	365	866
poi	168	101	98	81	127	119	104	104	55	34	46	46	53	47	23	25	47	35	58	62	16	12	795	666	1461
ct⁶ v wy²	13	21	22	8	24	13	15	7	7	8	3	4	10	7	5	4	7	3	10	4	4	4	120	83	203
f	20	12	22	13	16	15	9	12	8	5	11	8	12	5	6	3	8	6	8	3	0	2	120	84	204
ct⁶ v	12	7	17	6	14	11	7	7	0	5	8	6	4	3	3	3	8	7	4	5	1	1	78	61	139
wy² f	13	11	14	5	9	7	11	9	5	5	1	6	7	2	4	2	1	2	6	5	2	1	73	55	128
ct⁶	21	20	14	19	21	29	19	31	17	7	3	7	10	16	5	4	12	15	11	4	2	2	135	154	289
v wy² f	20	14	13	6	15	6	24	7	4	8	8	8	15	9	4	7	10	2	16	1	1	1	130	68	198
ct⁶ f	2	0	5	0	2	2	1	0	2	0	0	0	0	0	0	0	0	0	1	0	0	0	13	2	15
v wy²	1	1	2	0	0	0	0	1	1	0	0	0	1	0	1	0	0	0	0	1	0	1	6	4	10
ct⁶ wy² f	..	..	1	0	..	..	1	2	1	..	..	..	..	..	..	..	..	..	..	..	..	..	3	2	5
v	..	..	..	0	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	0	0	0
ct⁶ v f	..	..	..	1	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	0	1	1
wy²	..	..	..	..	..	..	..	..	1	..	..	..	..	..	..	..	..	..	..	1	..	..	1	2	3
ct⁶ wy²	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	0	0	0
v f	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	0	0	0
	347	268	291	192	329	272	253	219	132	98	112	111	156	110	68	54	126	93	135	104	26	26	1975	1547	3422

TABLE 31

$(X^4 \times svr^{poi\,h}) \times X^4$

Class	Number/broods																		Total		Total
	149/4		150/3		121/3		122/2		119/2		M 2/2		M 5/3		m 6/3		M 7/2				
	♀	♂	♀	♂	♀	♂	♀	♂	♀	♂	♀	♂	♀	♂	♀	♂	♀	♂	♀	♂	
ct⁶ v wy² f	89	60	76	68	111	70	63	45	57	52	61	32	40	23	94	67	91	71	682	488	1170
poi	152	138	159	113	155	131	68	83	71	79	107	91	122	104	154	165	93	97	1081	1001	2082
ct⁶ v wy²	19	13	16	17	26	18	16	16	19	9	18	17	9	8	28	25	17	14	168	137	305
f	21	14	24	20	25	13	15	17	13	11	8	13	16	16	25	19	22	12	170	135	305
ct⁶ v	15	16	11	15	16	17	6	9	3	5	13	8	4	13	27	19	14	17	109	119	228
wy² f	21	10	9	8	13	9	8	7	6	3	13	6	7	3	18	11	8	6	103	63	166
ct⁶	21	15	12	16	28	22	13	11	10	14	18	12	12	21	32	18	19	17	165	146	311
v wy² f	37	18	25	12	29	17	8	11	16	6	17	4	18	8	39	9	26	12	215	97	312
ct⁶ f	0	1	0	0	3	5	...	3	2	3	0	0	0	0	7	1	5	5	17	18	35
v wy²	1	1	3	5	4	0	...	...	2	1	1	3	2	1	4	2	1	4	18	17	35
ct⁶ wy² f	0	0	0	0	0	1	...	...	...	...	1	...	...	...	...	...	...	...	1	1	2
v	2	1	1	0	0	...	...	...	...	...	...	...	...	1	...	...	...	1	3	3	6
ct⁶ v f	0	0	0	0	0	...	...	...	...	...	...	...	...	...	...	1	...	...	0	1	1
wy²	0	1	0	0	1	...	...	...	...	1	...	...	...	...	...	...	1	1	2	3	5
ct⁶ wy²	0	0	0	0	0	...	...	1	...	...	...	1	...	...	...	...	...	...	0	2	2
v f	0	0	0	0	0	...	...	...	...	...	...	...	...	...	1	...	...	...	1	0	1
	378	288	336	274	411	303	197	203	199	184	257	187	230	198	429	337	297	257	2755	2231	4966

subsequent tests. It ought to be added that thus far no deficiencies at known loci have been found genetically in pointed, though such are known in the original px bl stock (see below); all available mutants between y and v were checked.

With these assumptions, it is to be expected that backcrosses with marked X chromosomes would give the following results: If both the second- and third-chromosome translocations are present in the autosomes of the pointed parents, F_1 females may be heterozygous for one or both of the autosomal insertions, or they may be normal if the pointed parent was heterozygous; the mother of the backcross will be heterozygous for the marked and pointed X. The X might be deficient for one or the other or both deficiencies. The expectation of lethal classes in the males of the backcross poi/X ple × X ple is that, in the absence of the transpositions in the first chromosome, ½ of the poi males will be missing in the plus class if one of the translocations is present, and ¾ if both are present. The same is true for the cross-

TABLE 32

CROSSOVER VALUES

	poi$^{px\ bl}$	poi	Standard
ct–v	12.2 ± 0.0056	14.2 ± 0.0050	13
v–wy	8.1 ± 0.0047	8.3 ± 0.0039	8.9
wy–f	12.7 ± 0.0057	13.9 ± 0.0049	14.8

over classes with the left end from poi. In the presence of the transposition, all the noncrossover pointed males are viable, but crossover classes in which the transposition has been removed by crossing over from the section containing the deficiencies show the possible ratios listed in table 29. (Half the males are always free of the deficiency and we assume that the very small duplications are viable.)

Tables 30–34 contain data on such a backcross, separately for the two pointed alleles. The marker stock was $X^4 = ct^6\ v\ wy^2\ f$, and the poi X was introduced by the father. As the left end was not marked, the noncrossover class ct–f contains also some single crossovers left of ct, and as the deficiencies are located near the svr region, about 17 per cent of male lethals are added to the noncrossover group. But in the other classes containing cut the error is negligible, because only double and multiple crossovers are involved. We did not tabulate here the individual broods, but added sister broods from the same F_1 cross (152/3 means 3 sister pair crosses from F_1 no. 152, all one-pair crosses). As table 32 shows, the crossover values are normal. In table 33 the sex ratios have been calculated for comparison with the expectations in table 29.

Keeping in mind the facts just pointed out, the summed-up results in all these tables show with perfect clarity that in the class v wy f about ½ of the males are missing, whereas the decisive noncrossover pointed class has an almost normal sex ratio. This latter fact excludes the presence of the 1→2 or 1→3 or both translocations as such, which would require a 1.33 or 1.6 sex ratio in the poi class. Therefore the lethal condition present in the v wy f class cannot indicate the locus of one of those deficiencies. It must mean that in addition to one or both translocations a duplicating transposition within the X chromosome must be present, inserted between v and wy. As the class wy f has also a high ratio, average 1.5, we must assume

TABLE 33

SEX RATIOS IN THE BACKCROSSES $(X^4 \times poi) \times X^4$

Class	SVR poi	SVR poi h	Both	Reciprocal classes, ratio normal : deficient		
				poi	poi h	Both
poi	1.18	1.08	1.12	1.26	1.18	1.21
ct v wy f	1.37	1.4	1.38			
ct v wy	1.44	1.23	1.31	1.44	1.24	1.32
f	1.44	1.26	1.32			
ct v	1.28	.9	1.06	1.3	1.16	1.22
wy f	1.31	1.63	1.5			
ct	.88	1.13	1.0	1.19	1.56	1.39
v wy f	1.91	2.22	2.1			
ct f	6.5	.9	1.5	3.17	1.0	1.32
v wy	1.5	1.1	1.13			
All	1.23	1.28	1.25			

TABLE 34

RATIOS ♀ : ♂ IN RECIPROCAL CROSSOVER CLASSES OF FORTY INDIVIDUAL BROODS FROM WHICH TABLES 30–33 WERE CONDENSED. RATIOS ARE UPPER LIMITS OF CLASSES OF .5 UNITS

(Frequencies of ratios n♀ : 1 ♂)

C.o. class	Ratio n♀ : 1 ♂															
	All ♂	0.4	0.9	1.4	1.9	2.4	2.9	3.4	3.9	4.4	4.9	5.4	5.9	6.4	6.9	7.4
ct v wy	1	3	8	10	6	3	5	3	..	1	..	..	..	..	..	..
f	1	..	10	15	3	5	2	3	..	1	..	..	..	..	..	..
ct v	2	6	6	17	6	..	..	1	..	..	..	..	1	..	..	..
wy f	..	2	2	13	4	12	..	1	2	1	..	1	..	..	..	..
ct	1	3	14	13	3	1	5	..	..	..	..	..	..	..	..	..
v wy f	..	2	4	9	4	4	2	..	2	2	..	1	..	2[a]	..	1
+ poi	..	1	11	23	3	..	..	..	..	..	..	..	..	..	..	..

C.o. class	Ratio n♀ : 1 ♂															
	7.9	8.4	8.9	9.4	9.9	10.4	10.9	11.4	11.9	12.4	12.9	13.4	14	15	16	All ♀
ct v wy	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..
f	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..
ct v	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..
wy f	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	1
ct	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..
v wy f	..	..	..	1	..	2	..	..	..	..	..	..	1	..	2	..
+ poi	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..

[a] All above 6 : 1 have only 1 ♂ each = 94 ♀♀ ♂.

that the locus of the transposition is about midway between vermilion and wavy. The relatively high sex ratio in the noncrossover ct v wy f class is, as already stated, the result of crossing over left of ct, which adds the deficiency near poi to this noncrossover class. Also, males with many recessive markers are less viable than females.

In the v wy f class the sex ratio is 2 : 1, and for both reciprocal classes it is 4 : 3. Looking at the table of expectations, we realize that this average result (after crossover elimination of the transposition) does not indicate which of the possible combinations were realized in the 40 individual broods from which the tables were derived, i.e., whether one or both transpositions were present. All it tells us with certainty is that not all broods could have been of the types which require a sex ratio of 4 : 1 or 1 : 0 in the decisive crossover class. Thus, it is important to check upon the individual broods which had an average size of 118 females 94 males. The individual crossover classes in single broods are not large, which involves a considerably higher error. But actually the crossover classes ct–v wy f contain a larger number of individuals than the classes ct v wy–f, and therefore a smaller error is expected, which makes comparison of the two more reliable. Table 34 is a frequency table for the individual ratios in the crossover classes. It shows at sight that the classes ct v wy, f, ct v, and ct have a similar range of variation of the ratios, whereas wy f and v wy f are different. These classes contain high ratios which obviously represent the expected 1 : 0 ratios with a few males left, which may be the result of double crossover between poi and the deficiencies. The other ratios may include the normals, 2 : 1 and 4 : 1 see table 29). This table, then, may be interpreted as showing: (1) that likewise in individual broods the transposition is never missing, since 2 : 1 and 4 : 1 ratios are absent in the poi class; (2) that in a number of broods (left end of the v wy f series) possibly no translocation is present, at least for the point near svr which is transposed to v–wy; (3) that in a number of broods one translocation is present, covered by a duplication in the v–wy region (ratio 2 : 1 of the v wy f series); (4) that in a number of cases both translocations are present and, as it seems, both left loci are transposed to the right end, one in the v–wy region, the other possibly to the right of wy (the classes around 4 : 1 in all c.o. classes with the right end); (5) that in ten cases the almost complete absence of males indicates the presence of homozygous autosomes without insertion (see table 29).

It may finally be added that sister R F_2 broods were also checked with respect to whether such sibs showed similar ratios in the individual broods. Looking at the ratios in the v wy f class, we found 8 such sibs of 2 or 3 broods, each, all of which had low ratios around 2 : 1 or 4 : 1.

The foregoing analysis was made with crosses in which the poi X was introduced by the father of F_1. As we found that females may have differently constituted X chromosomes (see the y crosses), a similar series was made by introducing the poi X via the mother, i.e., $(\text{poi} \times X^{y}) \times X^{y}$. Tables 35–39 show the results. Table 35 contains the summarized results for 25 broods each for poi and poi h, including the sex ratios of the larger classes; table 36 contains the crossover values; and tables 37–40 contain special data for the analysis of individual broods.

We notice first that the noncrossover class + (poi) is practically equal for both alleles in both sexes. The X^{y} noncrossover class is four times as large in poi h as in poi. This class with 7 recessives is, of course, very little viable. But this inviability

TABLE 35

CROSSING OVER IN THE poi × X^{7} CROSSES

Class		poi		poi h		Sex ratio	
		♀	♂	♀	♂	poi	poi h
svr (= poi = svr^{poi})		751	568	767	566	1.32	1.36
Single	y ec ct v wy f car	18	16	78	65	1.12	1.20
	y	26	40	9	14	0.65	0.64
	svr ec ct v wy f car	5	1	6	1	....	....
	y ec	22	38	63	56	0.58	1.12
	svr ct v wy f car	10	7	59	11	1.43	5.36
	y ec ct	17	21	41	68	0.81	0.60
	svr v wy f car	30	7	96	31	4.29	3.10
	y ec ct v	10	14	23	21	0.71	1.10
	svr wy f car	72	8	53	18	9.00	2.94
	y ec ct v wy	6	4	22	19	1.50	1.16
	svr f car	95	29	77	23	3.28	3.35
	y ec ct v wy f	18	13	22	10	1.38	2.20
	svr car	62	36	54	34	1.72	1.59
Double	y car	3	1	3	..	....	....
	y f car	4	2	3	1	....	....
	svr ec ct v wy	2	..	3	..	....	....
	svr ec ct v	..	..	3	..	....	....
	y v wy f car	3	..	1	..	....	....
	y ec car	3	1	6	8	....	....
	svr ct v wy f	1	1	5	1	....	....
	y ec f car	1	1	11	13	....	0.85
	svr ct v wy	5	3	22	7	....	3.14
	y ec wy f car	..	..	1	1	....	....
	svr ct v	3	2	13	5	....	2.60
	y ec ct car	..	..	3	3	....	....
	svr v wy f	2	1	9	1	....	9.0
	y ec ct f car	..	..	3	2	....	....
	svr v wy	12	5	28	12	2.40	2.33
	y ec ct wy f car	1	1	2	..	....	....
	svr v	..	..	..	1	....	....
	y ec ct v car	3	..	2	1	....	....
	y ec ct v f car	1	..	5	..	....	....
Triple	svr ec ct car	..	..	1	..	....	....
	y ec ct wy	..	..	1	..	....	....
	y ec v	..	..	1	..	....	....
Sa.		1186	820	1496	993	1.45	1.51

is increased in poi (and, as we shall later see, also in px bl), showing that poi contains other debilitating features in the autosomes enhancing this inviability. Whatever differences we find thus between poi and poi h aside from this inviability are based upon different genetical features.

A look at the crossover values in table 36 shows at once that there is a considerable difference between the two svr alleles. In poi there is a large reduction of crossing

over from yellow to vermilion, aside from the sexual differences. A look at tables 35 and 37 shows one of the reasons for this difference, namely, the reduction of double crossing over in poi as compared to poi h, in addition to that of single cross-

TABLE 36

CROSSOVER VALUES (poi AND poi h × X^7) × X^7 = y ec ct^6 v wy^2 f car

Segment	poi		poi h		Stand.
	♀	♂	♀	♂	
y–ec	3.6	5.4	1.9	1.6	5.5
ec–ct	3.8	6.5	12.1	10.3	14.5
ct–v	5.5	4.3	12.2	10.0	13.0
v–wy	7.6	3.0	7.6	4.7	8.9
wy–f	10.6	5.4	12.4	7.7	14.8
f–car	7.8	6.5	7.0	5.8	5.8
svr–ec	....	0.23	....	0.2	5.4

TABLE 37

SINGLE AND DOUBLE CROSSOVERS AS PERCENTAGES OF THE NONCROSSOVER poi CLASSES

Interval	Single crossover				Double crossover			
	poi		poi h		poi		poi h	
	♀	♂	♀	♂	♀	♂	♀	♂
y–ec	4.1	7.2	1.9	2.6	1.6	0.5	1.8	0.2
ec–ct	4.3	8.0	17.2	12.4	1.7	1.4	7.7	6.4
ct–v	6.3	6.7	17.2	17.5	2.4	1.2	6.0	3.5
v–wy	10.9	3.9	10.0	6.9	1.1	0.5	3.7	1.4
wy–f	13.5	5.8	12.9	7.4	3.3	1.9	10.0	6.4
f–car	10.7	8.5	10.0	7.8	1.6	0.7	3.8	2.5
Totals	49.8	40.1	69.2	54.6	11.7	6.2	33.0	20.4

TABLE 38

SEX RATIOS OF NONCROSSOVER poi CLASSES

	Ratio											
	Below 1	-1.3	-1.6	-1.9	-2.2	-2.5	-2.8	-3.1	-3.4	-3.7	-4.4	45 : 1
Frequency poi h	6	8	2	1	2	1	1	1	..	..	2	1
Frequency poi	5	9	4	3	..	1	1	..	..	..	1	..

ing over. In view of the identical sizes of the + poi classes, these values ought to parallel each other if the X chromosomes are constituted identically. In table 37, therefore, the individual single and double crossover individuals have been calculated as percentages of the noncrossover poi class, both for poi and poi h, and for all intervals. A comparison with the crossover table 36 shows: (1) Single crossing over is reduced considerably in the y–ec interval of poi h, but not of poi; double cross-

over breaks are nearly similar, thus showing fewer double crossovers in poi. (2) In the interval ec–ct crossing over is about normal in poi h but much reduced in poi; table 37 shows that both single and double crossovers share in this reduction. (3) In the interval ct–v, again, poi h shows almost normal crossover values, and poi much

TABLE 39

SEX RATIOS IN SINGLE CROSSOVER CLASSES WITH MISSING MALES, CORRELATED TO THE SEX RATIO OF THE NONCROSSOVER poi CLASS

Single crossover class	poi Sex ratios of the noncrossover poi class								
	Below 1.3 (14)			1.3–1.8 (7)			Above 1.8 (3)		
	♀	♂	♀ : ♂	♀	♂	♀ : ♂	♀	♂	♀ : ♂
v wy f car	12	2	0.6	12	3	4	4	3	1.33
wy f car	43	8	5.4	23	..	∞	6	..	∞
f car	64	21	3.0	26	3	8.7	5	7	0.7
car	34	17	2.0	25	12	2.1	3	3	1.0

Second column, test for transposition ratio 4 : 1 : $\chi^2 = 5.0$, $P < 0.05$; ratio 10.1 : 1, P.E. = 2.2, Dev. exp. ratio 3.2.

Total: all single crossovers with left end not from poi; poi h = 180 ♀ 188 ♂, poi = 99 ♀ 132 ♂. The same with left end from poi; poi h = 345 ♀ 128 ♂, poi = 274 ♀ 88 ♂. The only large double crossover class v wy has, all together, 12 ♀ 5 ♂ for poi, 28 ♀ 17 ♂ for poi h.

TABLE 40

(Continuing from table 39)

SEX RATIOS IN SINGLE CROSSOVER CLASSES WITH MISSING MALES, CORRELATED TO THE SEX RATIO OF THE NONCROSSOVER poi CLASS

Single crossover class	poi h Sex ratios of the noncrossover poi class											
	Below 1.3 (14)			1.3–1.9 (3)			1.9–3.1 (5)			Around 4 (2)		
	♀	♂	♀ : ♂	♀	♂	♀ : ♂	♀	♂	♀ : ♂	♀	♂	♀ : ♂
v wy f car	59	22	2.7	3	..	∞	7	3	2.3	6	..	∞
wy f car	33	16	2.1	3	..	∞	4	1	4.0	4	..	∞
f car	49	18	2.7	7	1	7.0	4	2	2.0	9	1	9
car	41	22	1.9	2	3	0.7	4	5	0.8	2	1	2

Fourth column: $\chi^2 = 1.8$, $P > 0.10$; ratio 10.5 : 1, P.E. = 1.3, Dev./P.E. = 2.3.

reduced ones; again, the relative share of single and double crossovers is not very different in both cases. (4) In the interval v–wy, crossing over is normal in the females and reduced in the males of both alleles. There are relatively more double crossovers in poi h. (5) In the interval wy–f, again, crossover values are about normal in females and low in males. In both sexes more double crossovers contribute to the results in poi h. (6) In the interval wy–car the same is true. (7) The sum total in table 37 shows clearly that altogether single crossover is about 25 per cent less frequent in both sexes of poi as compared with poi h. Double crossing over is about three times as frequent in poi h has in poi, so that the scarcity of double crossing

over is mainly responsible for the low crossover values in the female and male classes of poi visible in table 36. Thus we see disturbances of crossing over:

for both sexes in ec–v of poi, not poi h
for males only in wy–f of poi and poi h
for both sexes in y–ec of poi h only
for none in f–car of both alleles.

Of these disturbances those located in the v–f interval act differentially in poi by the reduction of survivors from double crossing over. Those in the interval ec–v act in poi differentially by reducing both single and double crossover. Thus we expect in the interval v–f a disturbance affecting the males of both alleles, and a difference between them affecting double crossover survival in both sexes. In the interval ec–v only poi contains a disturbance affecting both single and double crossing over. Also, poi h had another disturbance affecting crossing over in the y–ec interval.

In table 36 the svr–ec crossover value is also found, taking into account that svr cannot be distinguished in the presence of yellow. The percentage is very small. We remember (see p. 299) that in addition to the well-known crossover irregularities at the left end of the X chromosome the values calculated for the poi stock are rather erratic.

Returning now to the crossing-over data summarized in table 35, we find that the sex ratios are about normal, even sometimes in favor of the males in the noncrossover classes and in all crossover classes not containing the left end of the original poi chromosome, but that they are high or very high in the reciprocal classes. Simple sex-linked lethals are excluded, and we must again think of translocations and transpositions. For simple translocations alone from X to an autosome producing ½ male lethal deficiencies in each case the expectations have already been tabulated (table 29), namely, 2 : 1 and 4 : 1, respectively, in the poi class and the proper crossover classes. Clearly, the poi class with large numbers does not show this ratio. But neither does it show a 1 : 1 ratio. This suggests that the 25 resp. 24 individual broods of which the poi and poi h crosses are composed may be different, i.e., the original-stock females may have been heterozygous with respect to the features studied here. Therefore we tabulate the frequencies of sex ratios found in the noncrossover poi class in table 36. The table indicates that the poi class contains a mixture of sex ratios, with a majority of cases 1 : 1, and a minority of 2 : 1, and 4 : 1 in both cases. There is one additional brood in poi h crosses with a single poi male among 46. This completely abnormal brood contains only 5 males altogether, with 67 females. With the exception of 2 females in the y ec class, all remaining 21 crossover females are found in the crossover classes containing the left end of the poi chromosome. The most probable explanation is that the poi X chromosome contained a lethal mutant (not present otherwise) and that another lethal mutant had arisen in the X of the tester stock, thus also permitting female lethal combinations. As these were present in all classes to the right of ec, i.e., absent in the y–ec regions, whereas the absence of males characterized all classes with the same region from poi, the new lethal in the tester chromosome must be located to the right of ec and the one in the poi chromosome to the left of this point. As one male poi survived, which must have been owing to crossover between svr and the lethal, the latter would be located even to the left of yellow. The four other surviving males (two each) were found in the y ec ct and v wy f car classes, which would suggest that the new lethal in the tester

chromosome was located between ct and v. But this would require also double crossing over between svr and the lethal. The explanation is unsatisfactory and the case has not been followed up.

To return to the other members of this series: If the ratios of 2 : 1 and 4 : 1 in the poi classes are significant, the two translocations studied above must have been present in some of the crosses, whereas the majority did not contain them. If in the latter group, however, typical aberrant sex ratios are found in definite crossover classes, we suspect again the transposition in the X chromosome which we had to assume before. Therefore (table 39, 40) we separated the data for the single crossover values in accordance with the ratios found in the noncrossover poi class. (Only a few double crossover classes have sufficient numbers.)

In the table the first columns for both alleles contain what probably is a 1 : 1 sex ratio for the noncrossover poi classes, which means either no translocations and transpositions, or deficiencies by translocation covered by transpositions, or only transpositions. In the first case, the crossover sex ratios should be normal. In the second case, they should be normal for the classes containing the right end of the poi chromosome (supposed to contain the transpositions) but deficient with only the left end of the poi X, namely, 2 : 1 if only one translocation-transposition is involved, 4 : 1 if both are present. In the third case, all males with only the left end from poi should be missing. The data for poi (first column) suggest clearly that both translocations and transpositions are present, and, further, that one of the transpositions is located in the v–wy region and the other right of the ca region. The abnormal ratios in the class which also contains ct (not found in table 39, 40) locate the deficiencies again in the left end.

The column for poi h shows different results. Here all crossover classes with only the left end of the poi X have a ratio around 2 : 1. This shows that only one of the translocations is present, covered by the transposition in the ca region.

In the event of high ratios for the noncrossover poi class (2 : 1, 4 : 1), one or both translocations must be present. In the absence of transpositions, all classes with the left end from poi must show the same ratios as the noncrossover class. In the presence of transpositions, the expectations are the same as before, as is exemplified in the classes with normal ratios for poi. Unfortunately, the numbers are rather small for these rarer groups and do not permit of a decision. The two groups for a probable 2 : 1 ratio in poi, i.e., either one translocation alone or both plus one transposition, seem rather alike, and, if added (columns 3 in poi and poi h), may represent a 4 : 1 ratio for the first two crossover classes and a 2 : 1 ratio for the others. This would mean two translocations with one transposition in the v–wy region. There are, further, two columns with poi ratios between 1 : 1 and 2 : 1 (second columns). The ten broods therein may belong partly to the one or partly to the other class. In the poi h group it seems probable that they belong mostly to the 2 : 1 class, though the numbers are too small for a decision. In the column for poi the first and the last crossover class agree with the results of the first column. But here we find no males in the wy f car class, and only a few in the f car class, a result which we would expect only if a transposition and no translocation were present, the transposition being located between wy and f (see statistical test in tables 39–40).

There are, finally, the two poi h broods with a 4 : 1 ratio for the poi class. Here two translocations and no transpositions ought to be present, and there should there-

fore be a 4 : 1 ratio in all cross over classes of the table. The small numbers may permit this explanation. Altogether we may conclude that the poi stocks may contain translocations from the left end of the first chromosome into the second, the

TABLE 41

svr$^{poi\,h}$/ec, a px sp/+ × ec, a px sp/a px sp

	♀	♂	Normal expectation	
			♀	♂
+	120	5	1	C.o. poi–ec
poi	..	127	..	1
ec	96	99	1	1
a px sp	78	5	1	C.o. poi–ec
ec, a px sp	116	71	1	1
poi, a px (sp)	..	31	..	1
poi ec	..	..	..	C.o. poi–ec
poi ec, a px sp	..	..	..	C.o. poi–ec
Σ	410	338	No crossover a–sp found	

third, or both, and in addition duplicating transpositions of the same left-end loci, one into the v wy region and another beyond car, and also that the possible viable combinations of all these may be present.

TABLE 42

svr$^{poi\,h}$ +/+ v, a px sp/+ × v/ a px sp/a px sp

Class	♀	♂	Normal expectation	
			♀	♂
+	103	14	1	½ c.o. poi–v
poi	..	48	..	1
v	76	71	1	1
a px sp	59	25	1	¼ c.o. poi–v
v, a px sp	74	42	1	1
poi, a px (sp)	..	33	..	1
v, a px	10	19	..	½ c.o. px–sp
v, sp	9	2	..	½ c.o. px–sp
poi v	..	8	..	¼ c.o. poi–v
poi v, a px (sp)	..	7	..	¼ c.o. poi–v
	331	269		

It is rather unfortunate that tests made with a large number of mutant loci never revealed the presence of known loci in the deleted or translocated sections. Thus a more detailed analysis was made impossible. But a few tests were conducted with two marked chromosomes in which the decisive regions in the first, second, and third chromosome were marked, namely, by echinus (ec) near poi, near which the deficiencies by translocation are supposed to be located; vermilion (v), which is near the transpositions in the first chromosome; a px sp in the region of the second

chromosome insertion, simultaneously a safe mark for pointed because of speck suppression; ebony (e), not far from the region of insertion in the third chromosome. Tables 41–43 contain three such backcrosses with the expectations if everything were normal. The first backcross of $svr^{poi\ h}$/ec, a px sp/+ × ec, a px sp/a px sp shows the expected number of females except that the class a px sp is rather small. This class has the composition a px sp/a px sp, poi +/+ ec. If the smallness of the class is significant—it actually recurs in cross no. 2,—and if it is not based on lower viability of the marked chromosomes, which is improbable in view of the perfect class ec, a px sp, crossing over in the first chromosome of the mother must be responsible. As ec is very near poi, many crossovers to the right of ec are expected

TABLE 43

$svr^{poi\ h}$ +/+ ec, +/e × ec, e/e

Class	♀	♂	Normal expectation	
			♀	♂
+	87	5	1	C.o. poi–ec
ec	86	76	1	1
poi	..	48	..	1
e	84	1	1	C.o. poi–ec
ec, e	70	73	1	1
poi e	..	29	..	1
poi ec	..	6	..	C.o. poi–ec
poi ec, e	..	..	..	C.o. poi–ec
	327	238		

which would produce backcross females without the transposition in the X chromosome, if present. These will be heterozygous both for the 1→2 and the 1→3 deficiency, which might impair their viability. But the decisive group are the males. The poi and ec males are present in the expected numbers. The class ec, a px sp males are just as deficient as the a px sp females. In this class it is possible that the duplication from 1→3 translocation and transposition is present in triplicate (via crossover beyond ec), which might account for lower viability. The class poi, a px sp is only about one-fourth of the expected size. In the presence of the 1→2 translocation, all, or almost all, males ought to be missing. But if the transposition is also present in the poi chromosome, all poi males ought to survive except for crossing over separating the transposition from poi. This is clearly the case in the small poi, a px sp class. But the same ought to be true for the poi class, which, however, is quite normal. This shows that only the second-chromosome translocation (and deficiency near poi) was present, and not the translocation to the third chromosome. A further check is furnished by the crossovers between poi and ec giving one-half plus, mostly with the transposition, if the deficiency by transposition is located near svr, and one-half poi ec without the transposition. The latter ought to be lethal with a px sp but for double crossovers. Actually, five crossover males each are found in the plus and a px sp classes, and none in the two poi ec classes. Thus the data fit our former analysis fairly well, indicating that by chance a poi chromosome with only the deficiency by translocation into the second chromosome was used.

In the second cross (table 42), in which ec is replaced by v, the females show approximately the same results as in no. 1. As vermilion is located almost 33 units to the right of pointed, considerable crossing over between the two is expected. In this case also some crossovers between a px and sp were found which had not appeared in the first cross. The percentages are near expectation for both. The summarized sex ratio shows at once that almost one-fourth of the males are missing. The majority of these are clearly contained in the poi and poi, a px sp classes. If we have our old translocations and transpositions, the poi class ought to be normal except for crossing over beyond v, between this and the transpositions, thus removing the transpositions from poi, i.e., making lethal all these crossovers combined with the unmarked third chromosomes which do not contain the translocation. The same is true also for the poi, a px sp combination where, in addition, the foreign second-chromosome combination (a px sp) is lethal when the proper transposition is removed by crossing over beyond v. Further, in the two small crossover classes, poi v one-half or all (with a px sp) ought to be missing because the transposition is absent, but for double crossovers between v and the transposition. Actually the numbers are much smaller than those for the reciprocal ++ classes. The fact that so many survivors are found in the poi v, a px sp class where only double crossovers can survive points to the transposition near ca as the one which is identical with the translocation into the second chromosome, the long intervals poi – v – ca permitting considerable double crossing over. There remains only the class v, a px sp (the small number of a px sp females has already been discussed with the former cross). Here a considerable number of males are missing. On the basis of our hypothesis these could be only double crossovers between poi–deficiencies–v, combining the deficiencies with vermilion without poi. On the whole, then the data confirm the interpretation.

The third cross (table 43) is parallel to the first but for the marking of the third chromosome. In the presence of both transpositions poi males ought to be normal. But all crossing over to the right of ec and to the left of the transposition will remove the transposition, whereas poi and the deficiencies remain, thus producing lethal poi. Actually, the poi class is far below expectation and still more so the class poi, e, where all the crossovers will die, whereas in the poi class only those with the homozygous second chromosome die. Among the crossovers poi–ec the poi–ec, e class must be lethal since the transposition is certainly absent, whereas in poi ec only half of the second-chromosome combinations will be lethal. Again the results confirm the interpretation.

The F_1 ratios.—This makes us return to the F_1 ratios reported above, namely, normal ratios in the crosses N × poi and $\underline{y}$ × poi, but variable abnormal ratios in the crosses poi × N (see table 12). In table 44 a number of possibilities for the constitution of the pointed female have been assembled, together with the resulting F_1 sex ratios. We did not assume homozygosity for the autosomal translocations, which, apparently are viable. They would lead to more normal ratios in the different classes, intermediate between those expected and normal. Homozygous deficiencies of the X chromosome are not expected to exist, though a case of complete absence of males occurred which might have been a case in point. The possibility of a single or double crossover between the loci of the two transpositions has been neglected. Such crossovers would further modify some ratios. Altogether, we expect to en-

counter most frequently ratios between 1 and 2, all over the range of this interval, further, ratios of 4 : 1 and many : 1—in agreement with the results in table 12.

Thus we may say that in a general way the experiments give consistent results, though there are incongruities in detail which indicate that the situation might be still more complicated. As the rearrangements are extremely small (see next section) and never could be shown to contain known loci, a further analysis does not look promising, and it would hardly be important for the problem which made us look into such minute details.

TABLE 44

SOME OF THE SEX RATIOS OBTAINABLE IN F_1 poi × N WITH DIFFERENT CONSTITUTIONS OF THE AUTOSOMES AND SEX CHROMOSOMES IN REGARD TO THE NONRECIPROCAL TRANSLOCATIONS 1→2 AND 1→3 (MARKED T), THE CORRESPONDING DEFICIENCIES IN THE LEFT END OF X MARKED Df 1–2 AND Df 1–3, AND THE LEFT–RIGHT TRANSPOSITIONS IN THE X CHROMOSOME CORRESPONDING TO THE TRANSLOCATIONS, MARKED Tr 2 AND 3. CROSSING OVER BETWEEN THESE TWO TRANSPOSITIONS IS DISREGARDED.

2d chromosomes of mother	3d chromosomes of mother	One X chromosome of mother	Other X chromosome of mother	Sex ratio F_1 ♀ : ♂
+/T	+/+	Df 1–2	+	1.33
+/T	+/+	Df 1–2 Df 1–3	+	1.60
+/T	+/+	Df 1–3	+	2.00
+/T	+/+	Df 1–2	Df 1–3	4.00
+/T	+/T	Df 1–2	Df 1–3	2.00
+/T	+/T	Df 1–2 Df 1–3	+	4.00
+/T	+/+	Df 1–2, 1–3 Tr 2, 3	+	1 + ¼ c.o. Df-Tr
+/T	+/T	Df 1–2, 1–3 Tr 2, 3	+	1 + ⅛ c.o. Df-Tr
+/T	+/T	Df 1–2, 1–3 Tr 2, 3	Df 1–2 Df 1–3	1.23
+/+	+/+	Df 1–2 Df 1–3	Tr 2, 3	2 − c.o. Df-Tr
+/+	+/+	Df 1–2 Df 1–3	+	2
+/+	+/+	Df 1–2	Df 1–3	No ♂♂ except ½ c.o. Df 2–3

The salivary-gland chromosomes of svr^{poi} and svr$^{poi\ h}$.—The cytological features of the svr^{poi} locus or region itself will be presented below, together with those of further alleles, because they cannot be described simply. Suffice it to say that the locus of svr, i.e., left of the break of a known deficiency, is normal. Here we present only the findings apart from the pointed locus or segment itself. The experimental results have already indicated that only very small sections could be involved, and further, that the individuals were not supposed to be alike in regard to the small deletions, translocations, and transpositions. Therefore, two types of checks were made. First, slides used for the study of the pointed locus itself were generally inspected for other regions. Secondly, a systematic check of a series of crosses and one-gland slides was made in the following way.[5]

[5] This check was made by Mr. Masuo Kodani under the supervision of the author. Later, many points were rechecked in the same slides by Miss Aloha Hannah, always with positive results.

A number of female as well as male poi and poi h were crossed to Oregon stock which had been checked for normality in the respective regions. From each cross a number of one-gland (one-cross) slides were made, and they were checked individually. In addition, a number of homozygous poi slides were made and checked for presence of the heterozygous condition of the respective rearrangements only. Thus a picture of the distribution of the rearrangements in the mutants was obtained. But only the positive results are important, since negative ones need not always mean absence when single or few bands, sometimes in difficult or unsuspected regions, are involved. The diagnosis given was derived from a comparison with the normal stock as well as with the published standard maps and was accepted only when the senior and junior authors gave identical interpretations. There is no doubt that the rearrangements to be described are present; but many others might have been found if the genetically unsuspected regions had been checked as thoroughly for single bands as were the regions indicated by the experimental results. The findings therefore represent minimum results. Altogether, 20 different small rearrangements were found with certainty, some of which, however, have a special meaning (see below). Tables 45 and 46 contain the condensed statistical data. The tables show that 12 out of 20 small rearrangements are found both in svr^{poi} and $svr^{poi\ h}$, which are of completely different ancestry, and further, that 4 in each were not found in this series in the other allele. Only a few of them have been found in all crosses, as the last column indicates. The rearrangements involve mostly one or two bands, maximum four. As was said before, only reliable cases were tabulated, and, with such small sections involved, this excludes a perfect record. But one might safely say that the actual occurrences will be roughly proportional to the findings. Regions with crowded small bands which are clearly visible only in case of perfect stretching may, however, contain too small a number of positive cases, in comparison with more favorable regions.

In the tables, the first column contains a description of the rearrangement. The next three columns indicate the number of pair matings for three combinations, and the fourth column, the number of one-gland—one-larva—slides made for all crosses; actually, in table 45, 15 slides poi × Ore, 70 Ore × poi, and 10 poi homozygous. The following columns indicate the number of glands in which the respective rearrangement was found, dubious cases being enclosed in parentheses. The last column contains information about the presence of the rearrangement in the 12 (in table 45) individual crosses. Table 46 is to be read in the same way. Furthermore, a column indicates where the individual occurrences are illustrated in plates 24–27.

There are in both tables a number of apparent rearrangements which we do not consider to be legitimate. All these are deletions and translocations of chromosome tips. These are numbers 1, 9, 10, 16 for poi, and 1, 9, 11, 15 for poi h. Their probable meaning has been discussed in a special paper (Goldschmidt and Kodani, 1943). An attempt was made to show that these are only pseudo-deficiencies and translocations, caused by artificial rupture of chromosome tips after attachment to each other.

In the X chromosomes of this series three deficiencies and two insertions were found: in $svr^{poi\ h}$, deficiencies nos. 3 and 4, and insertions nos. 2 and 5; in svr^{poi}, the same insertions (nos. 2 and 4), but only one deficiency. The no. 2 insertions were different in the two alleles, with only one band in svr^{poi} and three in $svr^{poi\ h}$. This latter insertion is located to the right of 3C7, i.e., between facet and echinus. A

different aspect of this insertion is presented in plate 28, fig. 5. As the table indicates, this insertion was found in almost every gland. For some time, it actually misled us into believing that this was a translocation of the speck locus and that pointed was this translocation; later, it turned out that pointed was a svr allele with the sp suppressor action found in other suppressors of the same region. As the genetical results made us expect a lethal deficiency in this general region (though not necessarily at this point), but no translocation or transposition, the section was studied over and over again; but there was no doubt that we saw an actual insertion. As has already been mentioned, this insertion may be considered as always present in both alleles, though its size is different in both. The insertion is not easily studied, because for an inexplicable reason the group of thick and thin bands of the w–fa region are invariably contracted into a thick chromatic mass (only in the poi slides, not in controls) in which the bands are hardly recognizable. The insertion which follows the fa band is usually included in this mass. As far as could be made out, there are three bands in $svr^{poi\ h}$ and one in svr^{poi}.

Looking over tables 45, 46, we realize that, with the lone exception of the pseudo-translocations of chromosome tips, this is the only rearrangement which is ubiquitous in both alleles; and we may add that this insertion is always absent in px bl (as well as Oregon), though many of the other rearrangements were also found in px bl. This insertion, then, must have played some role in the independent origin of the two pointed alleles! We did not succeed in finding out with certainty where it comes from. No synaptic association with another chromosome was observed, and no such association with another part of the X which could point to a transposition. Actually there is a deficiency, only in poi h, in section 4 of the X chromosome (no. 3, table 45) the three bands of which correspond to those of the insertion, and this locus is near 10 of the genetic map, i.e., between ec and cv. Is it possible that one of the two transpositions from left to right which the genetical data indicated is actually from right to left? The crossover experiments ought to give such information, but the facts could never be interpreted thus.

It ought to be repeated that the insertion is not easily studied. In all slides of the poi series, though not those of the controls, the group of conspicuous bands to the right of which the insertion is located (the white–roughest–facet group) tends to contract into an X-shaped mass of chromatin which can hardly be analyzed. The tiny inserted bands tend to disappear in this tangle. But when the fa band is clearly separated, the insertion also becomes visible between this and the broken band to the right, both of which are easy to recognize.

The only other chromosome abnormalities found in the X chromosome of both alleles is a deficiency (no. 4, table 45, for poi h) of two bands in section 9, to the left of vermilion. This is not expected on the basis of the genetical data, though some of them which have been interpreted differently might be connected with this deficiency, which was found in 7 out of 12 crosses. (We shall meet later with a vermilion deficiency in px bl). Plate 28, figure 7, shows this deficiency in a well-stretched and not synapsed chromosome section. But the main failure of the cytological check is that the transposition between vermilion and wavy indicated by the genetical tests was not regularly found. A one-band insertion at 12 E, i.e., in the proper region, was actually found (table 46, poi h no. 5, and table 46, poi no. 4) in both alleles, but only three times in one gland each of 3 out of 12 crosses. This is not satisfactory.

TABLE 45

SALIVARIES OF SVR$^{poi\ h}$

No.	Rearrangement	Number of bottles (one pair)			No. of slides	Number of slides positive[a]			Plate and fig.	Remarks
		poi × Ore	Ore × poi	poi homo		poi × Ore	Ore × poi	poi homo		
						(15 slides)	(70 slides)	(10 slides)		
1	Df and T(X)1A1–4.....	3	7	2	95	6 ♀	36 ♀	.....	[b]	In all but 1 cross
2	T(X)3C.....	3	7	2	95	2 (8) ♀ 1	49 ♀	.....	25/2	In all crosses
3	Df(X)4C9 and 4D1, 2[c].	3	7	2	95	.....	5 (1) ♀	.....	23/4	Only in 1 cross
4	Df(X)9A2, 3.....	3	7	2	95	5 ♀	.....	2 ♀	25/1, 2	In 3 out of 4 crosses
5	T(X)12E.....	3	7	2	95	.....	1 ♀	.....	25/9	1 cross
6	Df(2R)48C5 and D5[c]..	3	7	2	95	.....	10 ♀♂	.....	24/5	Only in 2 crosses
7	Df(2R)53D8[c].....	3	7	2	95	.....	4 ♀♂	.....	24/6	Only in 1 cross
8	Df(2R)58D5.....	3	7	2	95	.....	12 (6) ♀	.....	26/1	Only in 3 crosses
9	Df(2R)60F4, 5.....	3	7	2	95	5 (2) ♀♂	8 ♀♂	.....	[b]	4 out of 10 crosses
10	T(2L)24AB.....	3	7	2	95	.....	5 ♀	.....	24/4	Only 1 out of 7 crosses
11	T(3L)61A.....	3	7	2	95	2 (2) ♀♂	17 ♀♂	6 ♀	[b]	In 9 out of 12 crosses
12	Df(3L)61C8.....	3	7	2	95	.....	.....	(2) ♀♂	26/2	Only 1 cross
13	Df(3R)86C6, 7, 8.....	3	7	2	95	9 ♀♂	8 ♀♂	.....	26/7	In all crosses with ♀ poi; in 2 out of 7 recipr. crosses
14	Df(3R)84D6, 7.....	3	7	2	95	.....	.....	.....	26/4	4 Found only in crosses outside of this series
15	T(3R)100F.....	3	7	2	95	6 ♀♂	45 ♀♂	3 ♀♂	[b]	In all crosses, 3 times in all 10 slides
16	Df(3R)91C4, 5.....	3	7	2	95	.....	.....	.....	26/3	Found only in crosses outside of this series

[a] Numbers in parentheses = probable but not certain cases. ♀♂ = found in chromosome of female and male larvae.
[b] Not illustrated ones have been published already by Goldschmidt and Kodani.
[c] Found only in poi h, not in poi.

TABLE 46

SALIVARIES OF SVR^{poi}

No.	Rearrangement	Number of bottles (one pair)			No. of slides	Number of slides positive[a]			Plate and fig.	Remarks
		poi × Ore	Ore × poi	poi homo		poi × Ore	Ore × poi	poi homo		
						(20 slides)	(5 slides)	(15 slides)		
1	Df(X)1A1–4.....	4	1	3	40	5♀	...	...	[b]	All of one cross
2	T(X)3C (diff. from poi h, fewer bands).....	4	1	3	40	16♀	1♀	...	25/7	In all crosses
3	Df(X)9A2, 3.....	4	1	3	40	3♀	...	2♀	25/1, 2	In 4 out of 8 crosses
4	T(X)12E.....	4	1	3	40	2♀	...	...	25/9	In 2 out of 8 crosses
5	T(2L)24AB.....	4	1	3	40	4♀♂	2♀♂	3♀♂	24/4	In 5 out of 8 crosses
6	Df(2R)58D5.....	4	1	3	40	6♀♂	...	3♀♂	26/1	In 4 out of 8 crosses
7	Df(2R)58E[c].....	4	1	3	40	2♀	...	1♀	24/7	In 2 out of 8 crosses
8	Df(2R)60D5, 6[c].....	4	1	3	40	1♀	1♂	...	24/8	In 2 out of 8 crosses
9	Df(2R)60F4, 5.....	4	1	3	40	2♀	2♂	...	....	In 2 out of 8 crosses
10	T(3L)61A.....	4	1	3	40	2♀	...	...	....	In 2 out of 8 crosses
11	Df(3L)61C8.....	4	1	3	40	3♀♂	...	2♂	26/2	In 2 out of 8 crosses
12	T(3L)70BC and 71BC[c]	4	1	3	40	...	...	3♀♂	....	In all homo poi
13	Df(3R)84D6, 7.....	4	1	3	40	7♀♂	4♂	8♀♂	26/4	In all crosses
14	Df(3R)86C6, 7, 8.....	4	1	3	40	7♀♂	4♂	8♀♂	26/7	Same as 13
15	Df(3R)91C4, 5.....	4	1	3	40	...	...	1♀	25/3	Only 1 homo poi
16	T(3R)100F.....	4	1	3	40	7♀♂	2♂	1♀	[b]	In 6 out of 8 crosses

[a] ♀♂ = found in chromosome of female and male larvae.
[b] Not illustrated ones have been published already by Goldschmidt and Kodani.
[c] Found only in poi, not in poi h.

The other transposition which ought to be located near the chromocenter was never encountered. But this, again, is a rather difficult region for very small disturbances.

In the second chromosome of svr$^{po^1\ h}$, 3 deficiencies were found in the right arm—leaving aside pseudo-deficiency no. 9,—but no insertion. The two infrequent deficiencies, nos. 6 and 7, are located in a region for which we have no genetical information. The third, no. 8, is the most frequent one and is present in both alleles in 7 out of 12 crosses, namely, the absence of band 58D5. This is the arc region. Since one of the alleles of the mutant broad angular is, as we shall see later, a deficiency of one (double?) band in this region, namely, 58D6, 7, and since the experiments indicated an insertion in this region, another investigation was made. Actually, a one-band insertion was found for svr$^{po^1}$, a little to the left, namely, between 58D2 and 3 (pl. 28, fig. 6). In svr$^{po^1}$ an additional two-band deficiency, 60D5, 6, was found in a few cases, located to the right of balloon. It is clearly derived from px bl, and it will be discussed in the section on px bl. In both alleles, furthermore, a one-band translocation was not infrequent in the left arm of the second chromosome between 24A and B, a region not far from dumpy. The origin could not be found, nor any genetic manifestation.

The third chromosome furnished quite a number of small rearrangements. Aside from the pseudo deficiencies and translocations at the tip, T(3L)61A, T(3R)100F, we found in svr$^{po^1}$ one deficiency and one translocation in 3L (nos. 11, 12), the latter not being present in svr$^{po^1\ h}$. The deficiency was rather frequent, the translocation less so. The deficiency is located near the free end (one band only) and might be responsible for the effects which we found located near ru h. The translocation, which was found only in homozygous svr$^{po^1}$, and here in all glands, is located near Lyra and Dichaete. As this is not far to the right of h, and as we found a powerful dominant enhancer of pointed in this region, we assume that this translocation represents the enhancer; enhancing actions of rearrangements are well known (see Goldschmidt and Gardner, 1942; Gardner, 1942). In 3R three deficiencies were found in both alleles. One of them was almost always present in both alleles, namely, Df(3R)86C6, 7, 8, which is a location between pink and curled. In some crosses with third-chromosome markers, not reported above, a lethal condition near cu seemed to exist, but the data were not unequivocal, and after some repetition with variable results we gave up further checks. The other, Df(3R)84D6, 7, was frequent in svr$^{po^1}$ and rare in the other allele. The location is to the left of pink, and no genetic effect was found. Another rare deficiency, Df(3R)91C4, 5, is located near ebony. The small translocation from X, which the genetic data required was found only once, namely, the insertion of one thick (double?) band in 91B (pl. 28, fig. 8).

Besides the disturbances found in this check series, a few more were observed which did not belong to this series. In the X chromosome a small Df(X)3D5—only one band—was found occasionally. The location is between fa and ec, both loci being known to offer abnormal genetic behavior. Further, in the region near the spindle fiber of 3R, where some small Df had been found, another was observed, Df(3R) 82E6 or 7. A number of these and other rearrangements found outside the test series are shown in table 4 and 5 (see legend).

b. THE MUTANT broad angular (bran)

In the general description of the first mutational changes, we mentioned a mutant broad angular (abbr.: bran) which appeared simultaneously with pointed and has reappeared many times since. We have already stated that the recombination of homozygous bran (i.e., broad rounded = broad angular, i.e., sometimes more rounded and sometimes more angular wings) with pointed homozygous or simplex produces a wing type described in my records as soft blistered. Some of the alleles of pointed can be best distinguished in this or a corresponding combination effect. Hence we shall first study bran, and afterward return to the other pointed alleles.

Phenotype and localization.—The original mutant showed considerably broadened, shortened, and rounded-off wings. In most of its later recurrences, however, the wings were not rounded but were more angular or squared at the tip. As extracted bran from crosses with the original stock also showed the angular type, modifiers must be involved. In some extracted bran groups the wings are still more angular at the tip and look like a transition to truncated wings. Again, modifiers seem to be involved, though we shall also meet with alleles which are characterized by the angular or dumpoid effect. The more rounded type resembles considerably the sex-linked mutant broad (br), though it is autosomal. A homozygous combination of both bran and br was made, which has an additive effect, still shorter and very broad, almost spherical wings. A very frequent feature of bran is upturned posterior scutellars. Further, some individuals occasionally have a small blister at the base of the wing. Their number may be increased by modifiers, as we shall see below, and, in addition, there is a combination of some bran and poi alleles which is characterized by such a blister (see below). Very rarely (1 in about 10,000) an individual looks like soft blistered (which contains svr^{poi}), but these, when tested, prove to be nothing but pure bran. When bran first appeared, there was a tendency towards short bristles, which, together with the smaller size of bran males (not females), produced a Minute-like effect. Later the bristles became and remained normal.

Though bran is a recessive, sometimes the heterozygote has somewhat broader wings, a dominance effect found in many recessives (e.g., bs, ba, px). In connection with another problem these dominance relations were studied in detail. The results are of interest in view of the origin of bran both from px bl and from svr^{poi}. A large series of different derivatives of px bl and pointed were crossed with bran and the dominance condition for individual broods was recorded in four classes : no, little, more, and high dominance. None of the tester stocks contained bran, but one contained arc, which acts as an allele of bran, as will be discussed below. Table 47 contains the data. This table shows that all crosses with different svr^{poi} stocks show hardly any dominance of bran; all the different px bl derivatives exhibit considerable dominance, and in two cases all broods have rather high dominance (all crosses made simultaneously under identical conditions and with long inbred stocks derived originally from one pair). The cross containing arc exhibits the allelism, with the additional feature of a lower phenotype of only the females in 6 broods. Obviously, dominance modifiers are involved, which, however, have not been analyzed further.

The localization of the mutant gave the following results. Crossover was checked

for the two dominant loci Lobe (72.0) and Bristle (54.8). Further, a combination of bran with ll sp was obtained by crossing over, the strange phenotype of which will be described below. This combination permitted an exact localization, as table 48 shows. This puts bran at or near the arc locus (99.2), a localization which

TABLE 47

F_1 N × bran

N	Broods	Grades of dominance (number of broods)				Remarks
		0	1	2	3	
1. px bl II	12	..	..	12	..	
2. px bl III	10	..	10	..	..	
3. px bl r	10	..	10	..	..	
4. px from poi × poi	11	..	11	..	..	
5. px extr	10	..	..	10	..	
6. px bl sel	10	..	10	..	..	
7. px low	9	..	6	3	..	
8. a px sp blist from 4	10	..	..	..	10	Allele! In 6 broods only ♂, ♀ in class 1
9. $svr^{poi\,h}$ I	10	10	..	..	..	But a few class 1
10. $svr^{poi\,h}$ II	12	12	..	..	..	But a few class 1
11. $svr^{poi\,h}$ III	9	9	..	..	..	But a few class 1
12. svr^{poi} I	12	12	..	..	..	But a few class 1
13. svr^{poi} II	11	11	..	..	..	But a few class 1

agrees with the phenotypic data to be recorded, and with the salivary analysis, which shows a one-band deficiency in this region for one bran allele.

The mutant arc has broader, flapper-like wings which are either arched or upturned. But the near-by locus plexus (100.5) also tends to have broadened, blunted wings. Bran was therefore combined in compounds with these loci and further tested opposite the Df(2)apx (or Ml). It behaved like an allele of arc, but there are

TABLE 48

Crossing-over Test for bran

	No.	C.o.	Per cent	Locus
C.o. Bl–bran	376	134	35.6	90.4+
C.o. l_2–bran	496	137	27.6	99.6
C.o. ll–bran	1338	109	8.14	98.56

a number of special features which will be discussed in another section below. On account of those features we did not speak of a^{bran}, but of bran.

Sex ratio.—The sex ratio within bran is normal. One count of pair matings gave 710 females 690 males. Only one of the broods had a 2:1 ratio and therefore contained a sex-linked lethal. Crossing bran females with Oregon males, an average sex ratio of 1491 females 1384 males was obtained. This was based upon the distribution shown in table 49. Comparing these ratios with those studied in poi, we see that in the long inbred bran line the different rearrangements have largely disap-

peared, but that some of them are still left in the stock. It did not seem worth while to repeat the analysis.

Combination with pointed.—Another remarkable feature of bran is its already mentioned recombination effect with poi. In the majority of cases in which it first appeared it was in this recombination. The usual effect (see below) of bran and poi homozygous together is a wing called *soft blistered.* The wing is shorter and more or less pointed and contains in the majority of individuals, usually in all, a large blister. Frequently, the wing is carried at angles to the body. Viability is lowered,

TABLE 49

SEX RATIOS bran × Ore

	Sex ratio						
	Below 1	-1.3	-1.6	-1.9	-2.2	-2.5	-2.8
Broods.....	6	13	6	1	1	1	1

but the true breeding stock is easily kept except when px is present simultaneously, as will be shown below. A certain percentage of the soft blistered flies, varying from none to about 20 per cent, show either one or both wings truncated, in extreme cases looking like an extreme rudimentary. But neither dp nor r is involved. Many selections for these truncate types were made, but only once (see below) were they somewhat effective, and in this case it was not the ordinary bran which was present. (Different bran alleles behave differently in this respect; see below). Obviously, these truncated wings are the result of competition between the pointed and the

TABLE 50

F_2 (poi × DIFF. bran)[2]

Class	+		poi		bran		soft blist	
	♀	♂	♀	♂	♀	♂	♀	♂
Number.....	258	223	141	150	40	50	67	51
Expected.....	♀ 379.5		♂ 355.5		63.3	59.3	63.3	59.3

broadening tendencies in development. This can be best demonstrated if bran is combined with lanceolate[2] (ll^2) by crossing over in the same chromosome. Such flies show at one end of a series of variations lanceolate, and at the other end truncate (dp or r-like) wings. The majority of individuals show all combinations of truncation with sharpening of the wing tips, different usually in right and left wings, in complete, more or less asymmetrical seriation from a lanceolate to a truncated wing. There is also a tendency toward arching in this combination. It ought to be added that both pointed and bran never show extravenation, though they are derived from a stock containing both px and bs. Soft blistered was synthesized by crossing both svr alleles to all the different bran stocks and breeding F_2 for the homozygous recombination, expected in one-eighth of the offspring. The result of such an experiment is shown in table 50 (nos. 5554 ff). The ratio 3 not : 1 bran and 7 not : 1 soft blist are rather good, though bran seems to be a little less viable. This was observed

also whenever bran was segregated in other crosses. This combination of bran and poi is very useful for the discovery of such pointed alleles, which otherwise are hardly distinguishable, and also for the analysis of position effects at the svr locus, as will be shown below.

The X chromosome.—It ought to be added that in all synthetic or analytic crosses involving soft blistered the possibility for abnormal sex ratios exists when the pointed X chromosome introduces the different deficiencies, translocations, and transpositions studied above. They are actually obtained, as the following example shows. (This fact tends to show that the second chromosome of bran still contains the small translocation from 1→2 near the arc locus, which is actually visible in the salivary gland chromosomes.) $Svr^{poi\ h}$ was crossed with bran, which simultaneously contained ll sp in the second chromosome. F_2 showed the segregation presented in table 51.

TABLE 51

$(svr^{poi\ h} \times$ bran ll sp$)^2$

♀				♂			
+	poi	bran ll sp	soft bl sp	+	poi	bran ll sp	soft bl sp
499	272	81	95	445	117	37	41
Exp. 3	3	1	1	3	3	1	1

As before, part of the pointed individuals are practically normal. The female ratio for not bran : bran (bran = bran + soft bl) is 4.4 : 1, which is probably due to the differential viability of bran. But in the males the ratio is 7.2 : 1. If we take the female classes as normal, half of the poi, soft blist, and bran ll sp males are missing. The male X chromosome may be in part a result of crossover, with all the chances for lethal classes discussed above for pointed. The total sex ratio is, as so frequently with pointed crosses, near 4 : 3, namely, 1.37. In another backcross soft blist × (N × soft bl) the sex ratio was 189 : 92, one-half poi males in all classes missing. Another cross, (soft blist × N) × soft blist, had a sex ratio of 568 : 410 = 1.38, with males again missing in the poi classes.

Since the detailed analysis of these ratios has been presented for poi, only a single check will be reported, namely, for the transposition in the X chromosome of pointed in the cross (X ple × soft blist) × X ple (table 52). All classes with the left end of the poi X but without the section near miniature (m) (m is located between v and wy) of the same chromosome are lethal for males. Adding these and their reciprocal classes, we get 35 female 41 male crossovers with either only the right part of the poi X beyond white or the left end plus the m region of the same chromosome; but 34 females 0 males in the reciprocal classes, i.e., left end of poi without its miniature region. This one check may suffice.

Modifiers.—One type of modifier ought to be mentioned because it produces a phenotype which cannot be distinguished from a certain other one which genetically is altogether different, namely, a combination of bran with another poi allele. (The check is of course a cross with poi.) It was stated above that occasionally some bran individuals have a blister at the wing base. In this case the wing is sometimes just a little sinuated at the posterior margin, like a beginning truncation. This type

is based upon an autosomal modifier in the third or fourth chromosome derived from px bl, which seems to contain it regularly. In a series of F_2 crosses (px bl × bran)², out of 1481 individuals 112 of both sexes had the type of wing described. This is roughly one-fourth of all bran segregants, indicating an autosomal modifier outside the second chromosome.

TABLE 52

1673–77 (X^g/Cl B × soft bl) × X^g

	Σ	
	♀	♂
+	82	71
X^g	17	..
y	..	1
w ec cv ct v m g f	..	..
y w	2	1
ec cv ct v m g f	..	..
y w ec	4	9
cv ct v m g f	3	..
y w ec cv	8	7
ct v m g f	7	..
y w ec cv ct	6	8
v m g f	10	..
y w ec cv ct v	..	2
m g f	6	..
y w ec cv ct v m	..	..
g f	..	..
y w ec cv ct v m g	..	..
f	7	3
y f	..	1
y ec cv v	..	4
v f	7	1
cv ct v m	1	..
y v f	..	1
y ec f	..	1
y w ec cv ct f	1	1
y w ec f	2	..
g f	3	..
ct v m	1	..
v m g	1	..
v m	1	..
Σ	170	112

Origin.—It was reported in the first section how the bran type first appeared simultaneously with pointed and rudimentary when the px bl line broke up (so-called mass mutation or upheaval). Later the same thing happened in a stock of a different px bl line. Since then bran has reappeared in various ways. Both px bl and poi stocks were checked all over again in large series of pair crosses, repeated from time to time, for the presence of bran (also poi in px bl), always with negative results. But rarely a single or a few soft blistered flies were found in svr^{poi} bottles, which, when checked, turned out to be homozygous for bran. Pure bran flies also

cropped up occasionally, i.e., flies in which bran had appeared as a mutant and pointed had simultaneously reverted to normal. The same thing has happened in constant and long inbred soft blistered stocks: a single bran fly was found by reversion of poi to plus; also in a stock with another poi allele. Further cases in which bran appeared in controlled matings will be reported and tabulated below, when we discuss the interrelation of all these happenings.

c. FURTHER pointed AND bran ALLELES

In the course of the work, other alleles of pointed and bran appeared, some easily distinguishable, others only traceable by their combination effects with bran.

The alleles svr$^{poi\ bl}$ and Bran.—The allele svr$^{poi\ bl}$ if isolated can hardly be distinguished from svr^{poi}; it is also a suppressor of speck. It is best recognized in the

TABLE 53

Patt × (Patt × poi bl)

[Patt = y, bw, e, ey]

	♀							♂							
Patt	bw e	bw ey	e ey	bw	e	ey	+	bw e ey	bw e	bw ey	e ey	bw	e	ey	+
19	12	7	9	32	36	3	39	10	13	18	18	19	17	21	23

plus + ey ♀ 42, ♂ 44
e + e ey ♀ 45, ♂ 35
bw + bw ey ♀ 39, ♂ 37
bw e + bw e ey ♀ 31, ♂ 23

combination with bran, i.e., bran/bran, svr$^{poi\ bl}$ flies (both sexes) are not soft blistered with short wings, but have long pointed wings with a blister, or, sometimes, a singed place instead, and are occasionally even indistinguishable from poi. This ellele (abbr.: poi bl, the combination with bran called pointed blistered or poi blist) is then more epistatic over bran than is syr^{poi}.

Its origin is rather complicated. We mentioned, in the Introduction, the appearance in certain crosses of a type with soft spread plexate and blistered wings (it is actually pointed blistered + plexus). It will be analyzed later, together with the discussion of the original happenings. A few individuals of this type were obtained in the following cross: 5891 B svr^{poi} × (svr$^{poi\ h}$ × svr^{poi}), i.e., a backcross between the pure silver alleles, neither of which was known to contain bran, px, or svr$^{poi\ bl}$ when the cross was made. We shall later discuss some such crosses that produced a reversion to px, which had been absent before. This backcross produced 40 females 35 males pointed, 1 female 4 males soft blist px spread. A pair of the latter type was mated, with the result: 6063 B = 5891^2 soft, etc.; 41 females 48 males poi, 16 females 12 males like parents, 2 males plexus, 5 females 2 males pointed blistered. Pointed blistered turned out to be heterozygous px, was isolated without px, and has bred true ever since. It contained bran homozygous and the new pointed allele. Thus, px, bran, and the new pointed allele arose simultaneously in a compound of svr^{poi}/svr$^{poi\ h}$. The meaning of this will be discussed in a special section. The poi blist stock was derived from this case; but the new allele has been found to reappear repeatedly (see below).

Pointed blistered was bred for many years. It never showed the short and fre-

quently truncated wings of soft blist, but varied in the amount of blistering. The location of the blisters differs from that in the px bl stock. The blisters are situated, not above the connection of the posterior crossvein with the fifth longitudinal, but either behind the crossvein in the fourth posterior cell near the posterior wing edge, or in the fifth cell. Sometimes a singed-looking area replaces the blister. Genetic tests showed clearly that the bran contained in poi blist is the same as studied before. F_2 from poi bl × plus segregates typically into 6 plus and poi, 1 bran, 1 poi bl. If both poi blist and soft blist are introduced together by a compound female, some F_2 segregates contain both soft bl and poi bl, thus showing the allelism of poi and poi bl. Otherwise the stock showed all the peculiarities of pointed with respect to modifiers and sex ratios, i.e., the different male lethal conditions described above.

TABLE 54*a*

Patt × (Patt × bran)

♀								♂							
Patt	bw e	bw ey	e ey	bw	e	ey	+	bw e ey	bw e	bw ey	e ey	bw	e	ey	+
56	50	60	72	106	91	51	154	66	84	70	73	113	112	39	144

♀ plus + ey 205
e + e ey 163
bw + bw ey 166
bw e + bw e ey 106

♂ plus + ey 183
e + e ey 195
bw + bw ey 183
bw e + bw e ey 150

One special feature was found for this allele which is worth mentioning. In making translocation tests with y, bw, e, ey (Patterson test) it was frequently noticed (see above, p. 319) that eyeless showed a lowered expressivity. We selected, therefore, a Patterson stock for high-grade eyeless, which gave more satisfactory results. But in crosses with poi blist we found the rather extreme results shown in table 53. The male segregation is normal (but for the usual tendency for smaller classes with increase of recessive mutants). But in the females the ey class is almost missing, and the bw ey and e ey classes are very small. But the size of the corresponding classes (ey–+, bw ey–bw, e ey–e) shows that the missing ey flies are contained in the corresponding class, e.g., in males 21 ey males + 23 plus males = 44, in females 3 ey + 39 plus = 42 females, etc. As the Y chromosome of the female is derived from the poi father, one might think of a Y→4 translocation with an effect comparable to Dubinin's cubitus interruptus effect. But a similar test with bran (not derived from poi bl) gave the results found in table 54*a*. Again while taking into account the different viability of multiple recessives, we find in the females little, if any, suppression of ey except in the plus and ey class. But now we find the same also in the males, which in this case do not have the poi X chromosome and have the Y derived from the Patterson stock. Thus it seems that the poi bl X prevents the ey suppressor action. Tests with cubitus interruptus were negative; hence we are inclined to assume that a suppressor action by some modifier and not translocation is involved in both cases.

A few years later the test for poi bl was repeated and only ey was checked, i.e., y, ey × (y, ey × poi bl). The classes not ey and ey were:

not ey : 196 females 144 males; ey : 22 females 57 males

The suppressor action which now worked in both sexes, though more so in females, then, is typical for the poi bl stock. This suggested a repetition for bran and for standard pointed. Soft blistered was used, which contains both. Simultaneously, another bran stock (marked 5087), which had arisen later, was tested. The results are contained in table 54*b*. As before, some of the ey effect was visible, but nothing comparable to the action of the poi blist stock. Therefore poi blist was tested over again, with the same results as before, which thus are proved typical. The explanation has been presented above, i.e., a dominant eyeless suppressor action located in the second and third chromosomes of this stock. This action seems to be additive when both second and third chromosomes from the poi bl stock are present in heterozygous condition. Furthermore, whereas the action may be found in different cases either in females only, or more extremely in females or in both sexes, it must

TABLE 54*b*

Cross	♀							
	Patt	bw e	bw ey	e ey	bw	e	ey	+
Patt × (Patt × soft bl)	19	34	18	20	30	19	15	49
Patt × (Patt × 5087 bran)	65	63	75	63	85	59	45	97
Cross	♂							
	bw e ey	bw e	bw ey	e ey	bw	e	ey	+
Patt × (Patt × soft bl)	16	10	15	13	17	16	20	42
Patt × (Patt × 5087 bran)	51	72	66	53	72	56	50	65

be assumed either that the X chromosome from poi, etc., more or less counteracts the suppressor effect, or that this effect tends—in a variable way—to work better in the female developmental system. If a suppression of eyeless by dominant suppressors is involved, the large not ey classes must contain many ey/ey individuals with suppression. Therefore a large number of RF_2 females from these classes were mated to brothers with eyeless (and bw or e). This was done for all cases in which the phenomenon was observed. The clearest results were expected in the case of poi blist, where the most extreme suppression of ey was found. F_3 should in this case contain a mixture of broods from ey/ey and ey/+ mothers. If we assume for F_3 about the same effect as found in F_2, we can calculate that the ey/ey mothers will produce about equal numbers of not ey and ey daughters; the ey/+ mothers about 3 not ey : 1 ey daughters. Among 25 broods, 13 had high ratios, altogether 337 not ey : 133 ey = 2.6 : 1; 12 broods had ratios near normal or even with an excess of eyeless, namely, 222 not ey : 275 ey = 0.8 : 1. We consider this a proof of the presence of suppressors in the second and third chromosomes. The other question, whether the absence or smallness of the effect in males is due to the specific X chromosome, is answered by a cross reported above (p. 318) (poi × bw, e, ey) × bw, e, ey. Half of the sons do not have the poi first chromosome, but they show the ey suppressor effect as much as the females do. (In this case, however, crossing over is possible). Therefore we must conclude that the poi X is actually responsible for the absence or covering of the effect in males. In order to make a comparison easier, we tabulate in table 55

all the backcrosses of the type under discussion and arrange the classes so that not-ey and ey classes follow each other in four pairs. In this table also, crosses are included which will be discussed below in connection with the additional ey domi-

TABLE 55

BACKCROSSES INVOLVING ey SUPPRESSION AND DOMINANCE

Cross	Females							
	bw e	bw e ey	bw	bw ey	e	e ey	+	ey
Control Oregon	73	68	87	58	81	62	89	73
Patt × (Patt × poi)	57	48	62	41	59	43	63	47
Patt × (Patt × poi h)	15	14	24	12	20	17	36	14
Patt × (Patt × poi s)	102	91	172	57	123	95	165	76
Patt × (Patt × poi blist)	12	19	32	7	36	9	39	3
Patt × (Patt × bran)	50	56	106	60	91	72	154	51
Patt × (Patt × bran 5087)	63	65	85	75	59	63	97	45
Patt × (Patt × soft blist)	34	19	30	18	19	20	49	15
Patt × (Patt × poi:dp)	22	55	63	24	42	36	67	35
Patt × (Patt × sl:dp)	2	19	23	13	13	8	29	11
Patt × (Patt × px bl II)	68	105	127	36	89	36	132	69
Patt × (Patt × px bl 4856)	51	52	60	48	38	47	83	36
(poi × bw e ey) × bw e ey	157	128	221	107	185	86	227	99
(poi × bw e ey) × bw e ey only ♂♂ not poi	..	..	..	..	..	..	..	..
bw e ey × (px bl × bw e ey)	53	66	88	58	83	79	116	59

Cross	Males							
	bw e	bw e ey	bw	bw ey	e	e ey	+	ey
Control Oregon	123	94	85	123	114	80	123	80
Patt × (Patt × poi)	34	44	55	56	58	40	76	66
Patt × (Patt × poi h)	16	14	23	17	18	21	22	30
Patt × (Patt × poi s)	44	90	129	117	79	77	191	111
Patt × (Patt × poi blist)	13	10	19	18	17	18	23	21
Patt × (Patt × bran)	84	66	113	70	112	73	144	39
Patt × (Patt × bran 5087)	72	51	72	66	56	53	66	50
Patt × (Patt × soft blist)	10	16	17	15	16	13	42	20
Patt × (Patt × poi:dp)	2	69	39	25	36	43	80	45
Patt × (Patt × sl:dp)	10	104	63	71	43	60	137	50
Patt × (Patt × px bl II)	80	67	102	89	111	85	135	80
Patt × (Patt × px bl 4856)	62	58	66	48	65	43	84	44
(poi × bw e ey) × bw e ey	63	130	156	118	125	67	142	88
(poi × bw e ey) × bw e ey only ♂♂ not poi	54	101	103	58	108	46	97	46
bw e ey × (px bl × bw e ey)	40	57	105	43	58	54	132	37

nance effect already mentioned, but most extremely represented in a stock to be analyzed later. Many different degrees of the effect (including absence of the suppressor in the second chromosome) are represented. F_3 tests for cases with a less extreme suppressor action were made in the same way as described above for poi blist. In a set of 53 F_3 broods in which the expectation for the female offspring of suppressed ey/ey and ey/+ was about 0.8 not eyeless to 1 eyeless and 2 not eyeless

to 1 eyeless, respectively, two clear-cut groups were found, namely, 32 broods with 559 not ey 235 ey = 2.4 : 1 and 21 broods with 357 not ey : 390 ey = 0.9 : 1.

We have already stated that the bran in poi bl which had originated simultaneously with this poi allele, just as the original poi had originated together with bran, behaved like ordinary bran when extracted or recombined with svr^{poi}. But twice this bran exhibited unusual behavior. In the first case, an F_2 (poi bl × ll sp)^2 showed

TABLE 56

3125 (poi^{bl} × ll sp)^2

	♀	♂
+ and poi	63	94
bran	9	13
ll sp	19	11
ll (sp) poi	26	5
poi bl	23	16

an abnormal segregation in so far as the bran class was too small, namely, no. 3725 (poi bl × ll sp).^{2} Expected: 4 + and poi, 1 each ll sp, bran, ll (sp) poi, bran poi = poi bl (results in table 56). The almost complete absence of ll (sp) poi males has been explained before by the translocation 1→2 near bran, which is derived from the ancestors of poi bl. But as bran is at least as viable as poi bl (though reduced in viability), the small number appeared significant. F_3 was therefore bred from a bran pair. The result is detailed in table 57. It shows—apart from the sex ratio—that the mother was heterozygous for poi, and further, that one of the parents had been heterozygous for bran though phenotypically bran. Also, most bran individ-

TABLE 57

4517. bran × bran FROM 3725

	♀	♂	
+	63	17	
bran	50	17	Bristles minute
poi	..	18	
soft bl	..	20	

uals showed a "Minute" type of short bristles. Further, no poi bl males, but soft blistered males, segregated. Obviously, a heterozygous condition of bran had arisen, with complete dominance and a bristle effect in the homozygote (compound) with bran. This compound together with poi produced soft blistered instead of poi bl wings. There is a strong suspicion that a bran deficiency had arisen of a size giving a kind of Minute effect including dominance, but viable opposite bran. A subsequent generation bred from these bran flies, which then are supposed to be compounds of the new and old bran, segregated into ½ bran and ½ almost bran, the latter with M bristles (4701). Another mass generation from this (4965) segregated again ll sp, showing that the incomplete bran in 4701 were heterozygous Bran/ll sp, and therefore that the parents bran 3725 had also contained Bran/ll sp and Bran/bran.

The final analysis of this new dominant Bran was prevented by a strange co-

incidence. In the last generation, 4965, a single crossover female ll sp and dumpy wings, also dwarfish, was obtained, but it was already fertilized when found. From this a stock was obtained, in 4 generations, homozygous for ll sp and bran in the

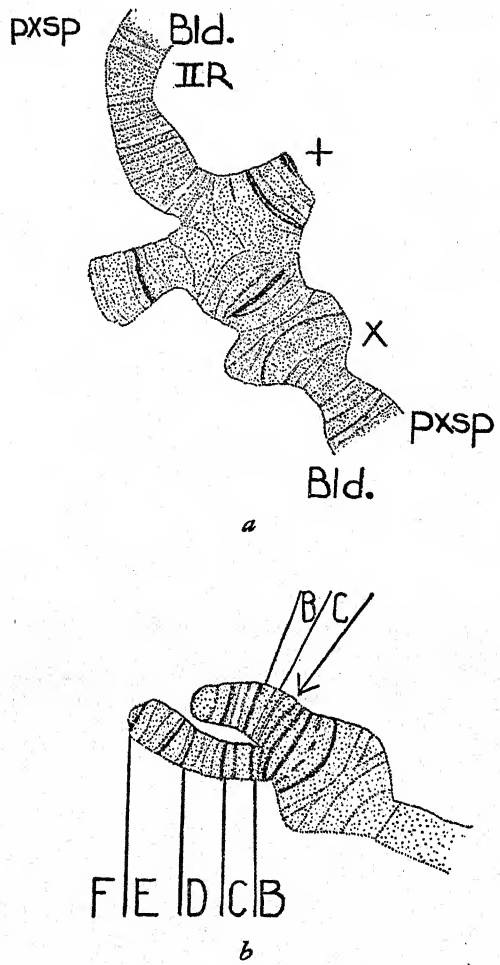


Fig. 1. Salivary gland chromosomes of T(1, 2)Bld heterozygous with px sp. *a*. The tip of 1 and the free end of 2R unite into the typical cross-shaped figure. Bld = X from Bld with attached tip at 2 of left. Upper px sp = second chromosome from px sp synapsed at left with translocated part from Bld-X. BldIIR = second chromosome of Bld with attached tip of 1, synapsed at right with X from px sp. *b*. The tip of X in Bld(1)Df. Above, the tip of normal X(1, ABC); below, the attached end of 2(60, B–F). M. Kodani del.

same chromosome, the phenotype of which was described above. Assuming that this was the new dominant Bran, the stock was kept for further tests. When the tests were made, it turned out that the stock contained the ordinary recessive bran and that the dominant had been lost. We shall later return to these crosses, since simultaneously with the dominant Bran there appeared also other mutants.

Once more, what probably was the same dominant Bran was produced after outcrossing poi bl, namely, to Blond translocation (Bld) in connection with the localization of bran. The overlapping of phenotypes requires a more detailed report, together with a few data on Bld which are missing in the literature on this translocation. Blond translocation is a reciprocal translocation between the right end of the second chromosome and the tip of the first. The breaks as studied by Bridges are reported in *DIS* 9, and text figure 1 illustrates the cytological facts. The tip of the first chromosome includes the svr locus. In the second chromosome the translocated piece does not include the bran locus, but the break is so near it that a crossover combination could not be obtained. The balanced Bld is known to segregate females and males with Bld(2) deficiency which have normal X chromosomes and a second chromosome with the translocated tip of X; Bld(2)Df is therefore simultaneously duplicated for the tip of X. Bld(2)Df are small individuals with spread and plexated wings, short bristles, and rough eyes. Bld(1)Df with two normal second chromosomes and one X with the translocation from II is therefore deficient for X but duplicated for the end of II; only females survive, males being lethal. The Bld(1)Df females are very large, blond, with very short bristles (varying from half length practically to absence, and have extremely broad wings, caused mainly by the enlargement of the fifth cell; sometimes the wings are arched; notching at the tip is sometimes found, also inflation of the wings. There is, further, a tendency toward abnormal tarsi and large rough eyes. These females hatch about 3 days later than their sisters. Bld(2)Df females are very rarely fertile, the males more frequently, and a considerable number of combinations with these males could be made. Bld(1)Df females are usually sterile, but offspring was occasionally obtained, the number varying from 1 to 20-odd, with many dead pupae in the bottle. Furthermore, the viability of both deficient types is poor, and they rarely appear in the expected numbers and frequently are completely absent. They are especially sensitive to the composition of the food. A special test made under good conditions and with special checks upon late hatchers produced the broods shown in table 58.

TABLE 58

CROSS: Oregon × Blond

No.	♀ Bld and ♂ +	(2)Df ♂	(1)Df ♀
4592	126	10	2
4593	108	12	6
4594	85	18	21
4595	84	5	5
4596	81	23	..
Σ	484	68	34
Exp.	484	242	242

A number of reciprocal crosses between Bld and poi bl gave the expected results. But one cross poi bl × Bld no. 3922 gave a very unexpected offspring; all daughters looked like Bld(1)Df, not so large as usual and less abnormal-looking, but otherwise exhibiting the broad wings and short blond bristles. All sons were ± pointed (±

meaning varying expressivity). In the next generation, females and males of the Bld,1)Df type appeared, though real Bld(1)Df males cannot survive. The males were also blond, broad-winged, and short-bristled, but rather small. A stock was established which bred true for females, the males segregating into the new blond type and soft blistered, when bred from blond pairs. This showed that poi and bran from poi blist were present in the latter males. Much work was done to find out what had happened. It turned out that neither the females nor the males were Bld(1)Df, which they resembled so much, but simply Blond translocation (balanced) but heterozygous for a bran allele. In this case again, Bran was dominant and made the Bld flies look like the (1)Df. In addition, the Minute-like tendency to short bristles which we met before with dominant Bran was present in this case, so that the Bld(1) deficiency effect was almost completely imitated, except for size. Unfortunately, a helper lost the stock before the salivaries could be tested, but there can be no doubt that Bran had appeared, probably as a larger deficiency. I repeat again that many similar crosses had only the expected results with recessive bran, which did not cross over into the Bld second chromosome and thus could not become homozygous. We shall return to these crosses, which also produced other mutants. Possibly the same dominant Bran appeared a third time in one of the mass changes in a px bl bottle. It will be discussed in a later section, in which an analysis of these happenings is to be attempted.

The alleles svr$^{poi\ sq}$ (pointed square) and bran^{2}.—The new allele of svr^{poi} was derived from the allele poi bl and, characteristically enough, again from a cross with Blond translocation, a sister cross of the one just reported. The expectation for F_2 (poi bl × Bld)^2 bred from Bld F_1 ♀ and poi F_1 ♂, both heterozygous for bran (from poi bl), is ¼ ♀♂ Bld, ¼ ♀ Bld(1)Df with homozygous bran (♂ lethal), ¼ ♀♂ Bld(2)Df with poi, ¼ ♀♂ poi blist. The actual result was: 10 ♀ 20 ♂ Bld, 1 ♂ Bld (2)Df, 3 ♂ of a new type: broad, very angular wings with blisters. The absence of most of the (1)Df and (2)Df is a frequent occurrence. But the absence of ¼ of poi blist ♀ and ♂, supposed to be at least as viable as the Blond translocation, is surprising, and has obviously to do with the appearance of the few males of the new type. These males were crossed to y and all sons were pointed; in F_2, ¼ of bran flies segregated in both sexes, and most of the bran males were blistered like the grandfather. The blister in this case has a tendency to be located near the base of the wing. The type has since been bred as a stock without change (marked 5121 broad blistered). It will be shown below that a new bran allele also is involved, bran^{2}. In both sexes the wings look like exaggerated bran, i.e., the tip is very broad and angular (therefore poi sq = square), with a tendency toward a beginning truncate. The majority of the individuals are blistered as described, but some are not. A similar blistering was described above as an occasional modification of bran. The new combination differs, however, from ordinary bran in the blunter wings and tendency to truncation. The new poi^{sq} thus is hypostatic to bran and shows its presence only in the blistering effect.

Checks showed that the Blond translocation had nothing to do with the new type. The homozygous bran which the new stock contained seemed to be the same (see below) as standard bran as tested in F_1 with +, bran, and arc. But it turned out later to be a new allele, bran^{2}, which shows a one-band deficiency in the salivaries. The bran^{2} svr$^{poi\ sq}$ stock (abbr.: bran blist) contained also some modifier for the

bran expression. The compound Df(2) a/bran^2 (from bran blist) has hardly any exaggeration effect, but in the backcross Df × (Df × bran blist) two types of compounds bran^2 Df appear in equal numbers, one like the F_1 compound, one with very broad, frequently nicked wings and much shorter bristles. As only one combination of the second chromosome is possible, the difference is based upon another modifier, which must be autosomal, since all males have the same X chromosome derived from the tester stock. A backcross bran blist × (Df × bran blist) shows the same modifying action. Among the Minute females (Df/bran^2), two types, a lower and an exaggerated one, are found. The same applies to the males, all of which have the same X chromosome. Among those with the Df/bran^2 compound (Minutes) also, a normal and a higher type are found, the latter with truncated blistered wings.

Thus the peculiar type of bran blist must be mostly based upon the pointed chromosome, which gives another combination effect with bran than the other alleles studied thus far. A first check is to introduce standard svr^{poi} into a combination with bran^2 from bran blist. This ought to give the typical soft blistered; which it does:

Control = (bran × bran blist)^2 = all ♀♀ bran, ½ ♂♂ ditto, ½ bran blist
Test = (poi × bran blist)^2 : ⅝ ♀♂ poi, ⅛ ♂ bran blist, ⅛ ♂ soft blist
Obtained: 72 ♀ 68 ♂ poi
7 ♀ 9 ♂ bran blist
20 ♀ 10 ♂ soft blist

If another locus in the X chromosome were involved, both crosses would have the same chance for crossing over, and thus some soft blist ought to appear in the control—which was not the case. Thus we have to assume a new allele of poi, namely, svr$^{poi\ sq}$, which, alone, has the same phenotype as pointed, but gives a different combination effect with homozygous bran^2. (Its sp suppressing effect is the same as in svr^{poi}). For salivaries see below. As has been repeatedly stated, it was later found that the bran contained in this bran blist stock was not the standard bran, but a new allele bran^2 which had arisen simultaneously with the poi allele. The proof will be furnished in the following section, where we shall meet with other new bran alleles.

The alleles svr$^{poi\ s}$ = soft and bran^1, bran^2, bran^{db}.—The recognition and analysis of the allele svr$^{poi\ s}$ has presented the greatest difficulties and involved a huge amount of work. The reason is its variable expressivity and its combination effects with a new allele of bran which originated simultaneously. This silver allele arose at one time within the plexus blistered stock without any visible effect, but became visible after outcrossing. In the course of the many years that this work proceeded, the px bl stock was tested over and over again in a large series of pair crosses with pointed and bran for the presence of these mutants, always with negative results (see below for details). The last extensive checks were made in 1942. But in a series of crosses px bl × N (N meaning different test stocks) made during the first months of 1938, the F_1 males with the X chromosome from px bl frequently had soft-textured, pointed-looking but not actually pointed wings, a type which could be isolated and bred as a sex-linked recessive. They were also pale and had the sp suppressor action of the poi alleles. At the same time, another type, called slender, with wings like lanceolate (ll, second chromosome), also sex-linked, as it seemed, segregated from similar crosses and could be isolated. It, too, had a tendency to soft-textured wings. Both types were isolated later again from other crosses. Their analysis was made possible mostly through the compound effects with bran. It turned out that "slender"

has the same pointed allele as soft wings, svr^{pois}, plus a new and weak allele of bran in the second chromosome, which has very little effect in the combination, i.e., is almost hypostatic.

This svr allele is of special importance because it was found at one time to be widespread in one of the unselected px bl stocks (called px bl II), thus showing that a pointed allele could originate here without becoming visible. (It disappeared later.) Furthermore, the simultaneous origin of a bran allele in px bl, again too weak to become visible by itself, is of importance. The facts must therefore be reported in more detail.

Soft wings are recognizable sometimes only by a certain sheen. In most cases the inner edge of the wings tends to be crumpled, and the wing tip is more or less

TABLE 59

PRESENCE OF THE ALLELE SVR^{POIS} IN px bl II, MARCH, 1938
F_1 px bl × SOMETHING

Mother	Number of F_1 broods with			Other ratios ♂ + : soft	All soft are folded	Most soft are folded
	♂ normal	♂ ½ soft ½ +	all ♂ soft			
px bl	4	4	10	38 : 9 36 : 14	1	1
px bl blist	5	5	22	47 : 15 32 : 11 48 : 18	..	2
Total	9	9	32	201 : 67		

pointed, which might easily be mistaken for the mutant pointed. (Both are pale, like all svr alleles.) In more extreme cases one wing is more or less folded. In the most extreme case both wings are rolled up like a wet towel. Frequently, a few individuals of this latter type are found among others; but in other instances every male without exception is of this extreme type. It is possible that these different types owe their origin to external conditions, though the frequent occurrence of a definite type seems to suggest a genetic causation by modifiers. Flies with soft wings tend to stick to the walls of the bottle, a fact which has to be reckoned with if counts are made. The soft individuals tended originally to have longer, softer bristles, a character which later disappeared. But in crosses with this allele, bristle abnormalties, such as V-shaped or forked bristles, are rather common.

The distribution of this allele in the px bl II stock in March, 1938, is recorded in table 59 for F_1 males of pair crosses px bl × something.

As the presence of the "soft" character is not visible in px bl (the pale color not being completely reliable in px bl females, better in males), the px bl males may be tested by crossing to attached X females. A series of 10 males from the same population thus tested gave normal males only once; in all other cases all were soft. Among these 9 broods, only 1 had ordinary soft wings; in 5 all wings were folded; and in 3 the majority were folded. All were pale. Heterozygous females are always normal, showing the character to be recessive. Obviously, the homozygous plexus

prevents the soft wing character from becoming visible. This might mean only that the strong plexation acting as a reinforcement of the wing makes the soft texture invisible (but see below), without affecting the pale color.

These results show that the majority of females in the population and almost all males were at that time homozygous for this recessive character; further, that homozygous normal females were very rare. (Cr. 1/5 of all cases.) In the px bl females the condition which produces the extreme folded type is relatively rare, whereas it is present in the majority of the males. Out of 14 heterozygous px bl females, 9 produced a 1:1 ratio of normal and soft-winged males, but 5 an exact 3:1 ratio. As only in two of these cases were about one-half of the males missing, this ratio is obviously due to a recombination with a "modifier." Actually, some of the not soft (though pale) males of this group transmitted soft in F_2, thus showing that only the phenotype was modified. This is, then, the same situation as was presented above for the pointed-wing phenotype of svr^{po1}. The table shows further that blistered and not blistered mothers produce the same types of sons.

F_2 from soft males gave, according to expectation, 1/2 plus, 1/2 soft of both sexes, and the recombination with homozygous px did not influence this condition. This is remarkable, as in the px bl stock the plexation obviously prevents the visibility of soft. But we shall see later that in F_2 from px bl crosses the low-type ordinary plexus appears, and not the strong plexation of px bl. This may mean that low plexation does not prevent visibility of soft, but it may also mean that the changed genetic situation after outcrossing (see below) is responsible for the visibility of soft with plexus. F_3 and F_4 from soft parents with or without px bred true.

The details of the data summarized in table 59 show that there is an additional relation between soft and the sex ratio, which, as will be shown below, is frequently abnormal in F_1 with px bl. In the cases in which px bl was homozygous for the absence of soft in the X chromosome, the F_1 sex ratio was normal, i.e., 378 ♀ : 352 ♂ = *ca.* 1:. When the px bl mothers were heterozygous for soft, a ratio of 773 ♀ : 561 ♂ was found, which is almost exactly 4 : 3, suggesting that 1 out of 4 males does not survive. The average ratio of normal to soft males in this case was 2 : 1 (298 : 149, not counting unreliable cases). The 1/4 of missing males thus belongs to the soft class. In the cases in which all F_1 males were soft and therefore the mothers were supposed to be homozygous for soft, the sex ratio in bottles carefully checked for males sticking to the bottle was 2150 : 759 = 2.8 : 1.

These sex ratios clearly indicate the presence—later proved—of the same translocations producing lethal classes as in pointed, which, then, seem to be essential also in the production of the new allele $svr^{po1\ s}$ (see below). Also, the same condition of the male X as in pointed (explained by a transposition) was found. The cross y, bw, e, ey × px bl gives soft or normal F_1 males and a normal sex ratio. The normal sex ratio for soft males indicates that px bl males containing a soft X chromosome are free from a lethal effect, seen when the X was derived from a female. But it cannot be excluded that the normal sex ratio is produced by the presence of both female and male lethal classes, the former caused by the presence of two foreign X_s. F_1 males of this cross, normal as well as soft and folded, were backcrossed to y, bw, e, ey, and again the sex ratio was perfectly normal in all cases, as well for the sum total as for the segregating classes. This shows the same condition in soft males as was encountered before in pointed. The soft stock was kept for many years, but its

phenotype changed toward something like pointed. But in outcrosses all the typical features remained, as will be reported. We repeat that all soft individuals are also pale and that they have also the speck suppressor action.

The type called slender, i.e., svr$^{poi\ s}$ + a new bran allele, was obtained in a different way, but also always out of crosses with px bl II performed in the same period, though not always involving the px bl X chromosome. Slender has a phenotype which is easily recognizable, especially when it is cleansed from modifiers by outcrossing. The wings resemble those of lanceolate[2], though they are not as narrow. They are very pointed at the tip, and the posterior edge shows the inward curving at the end of the fifth vein which characterizes lanceolate. The wing appears longer than usual because of its narrowness.

Slender appeared first from crosses involving px bl but made so that the X chromosome from px bl was not present, namely:

1st gen. no. 668 : + (Florida) × px bl ♂
2d gen. no. 913: bs × F_1 ♂, i.e., a male with an X chromosome from Florida, otherwise heterozygous with px bl. All offspring were giant with a normal sex ratio (for giant see later)
3d gen. no. 1147 = 913[2] giant : ♀♂ giants and intermediates, ♂ also dwarf; sex ratio normal
4th gen. no. 1264 = 1147[2] intermed.: 25 ♀ giant 9 ♂ intermed. (one dwarf) and soft wings
5th gen. no. 1363 = 1264[2] giant × soft: many ♀ normal, 2 ♀ 3 ♂ ski wings
6th gen. no. 1410 = 1363[2] ski: only 30 indiv., half ♀♀ are slender, all ♂♂ soft
7th gen. no. 1436 = 1410[2] slender × soft: all slender; breeds true (stock old slender)

A second appearance of the allele had similar features:

1st gen. no. 1935: px bl II × + (Oregon) part males soft; sex ratio 4 : 3 (made 1938 when soft was contained in px bl II)
2d gen. no. 2145 = 1935[2]: normal segregation, many ♀♂ soft wings
3d gen. no. 2145[2]: many giants
4th gen. no. 2297 = 2145[3] giants: size variable, half ♀♂ slender
5th gen. no. 2390/91 = 2297[2]: slender breeds true (stock 2297 slender)

In both cases, slender was derived from px bl II at a time when it was known to contain the soft allele. In both cases, the production of giants preceded the appearance of slender, i.e., a bran allele + soft. In the second case, soft was already present in the X chromosome derived from px bl. In the fourth generation via giants, slender appeared. Giant, then, had to do with the appearance of a new bran allele present in slender. In the first case, however, the X chromosomes were derived from bs or Florida stock. Nevertheless, in the fourth generation the X chromosome allele soft appeared from giant parents, and two generations later slender came from somewhat unusual parents (ski wings), showing that the bran allele had appeared again. The soft mutant, then, must have been produced here via an autosomal condition derived from px bl, a condition involved in the production of the giants as well as of the new bran allele (crossing over in the X chromosome being also excluded).

The new bran allele, bran[1], was found to be present in slender when slender and soft were compared in outcrosses with arc, bran, and the different poi alleles combined with bran. It turned out that soft alone behaved in crosses with arc like pointed, i.e., arc was simply recessive. But slender × arc produced flies with broader wings which could be described as almost bran, and further generations showed the same compound effect, though the homozygous new allele without soft could hardly be distinguished from normal. The same compound effect—almost bran—was obtained in crosses slender × bran (but not soft × bran). We saw, when studying the

TABLE 60

CROSSES WITH soft (svr^{pois}) AND slender (bran^{1}/bran^{1}, svr^{pois})

No.	Cross	♀ +	♀ soft	♀ poi sing	♀ poi	♀ sl	♀ bran	♀ soft blist	♀ dp blist	♀ poi blist	♂ +	♂ soft	♂ poi sing	♂ poi	♂ sl	♂ bran	♂ soft blist	♂ dp blist	♂ poi blist	Remarks
6625	sl × poi	..	..	..	All	..	..	..	..	..	..	All	..	..	..	..	..	..	..	
6626	sl × bran	81	..	..	..	..	..	..	..	..	..	31	11	..	..	..	..	..	..	♀+ are almost bran
6627	sl 2390 × bran	33	..	..	..	..	..	..	..	..	..	9	11	..	..	..	..	..	..	♀+ are almost bran
6628	sl × soft	..	10	21	..	37	..	..	..	..	..	52	1	..	..	..	..	..	..	♀vary between soft and slender
5512 ff	soft × bran	324	..	..	..	..	..	..	..	..	..	179	10	..	..	..	..	..	..	♂± poi
6951	soft × bran blist = bran^{2}/bran^{2}, poi^{wl}	..	..	..	..	30	..	..	1	..	..	19	4	..	..	..	..	..	5	8♀sl have one wing sl blist; 3♀sl other wing poi sing
6693	(sl × poi)^{2}	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	From poi via soft to slender, not classifiable
6695	(sl × bran)^{2}	24	15	..	22	..	13	10	..	..	34	17	..	..	6	10	12	..	..	sl are very slender and singed; + are almost bran
6696	(sl × bran)^{2} ♂ sing.	41	19	..	..	19	10	12	..	..	36	13	..	..	11	4	11	..	..	sl are very slender and singed; + are almost bran
6698 ff	(sl × soft)^{2}	..	..	76	..	88	..	..	..	..	..	..	19	..	82	..	..	..	..	♀all sl and sl sing; ♂ more like poi
5701/02	(soft × bran)^{2}	81	25	17	..	..	17	19	..	..	84	49	8	..	..	14	20	..	..	
7094 ff	(soft × bran blist)^{2}	..	..	22	..	95	..	39	..	37	..	..	15	..	97	..	20	..	9	♀poi sing = sl sing; ♀poi bl = sl blist; ♀soft bl = bran bl + soft bl; sl contains also soft
7097	(soft×bran bl)^{2} F$_1$♀dp	..	..	3	..	30	..	5	8	10	..	..	4	..	28	..	10	2	6	
5715/16	(soft × bran bl)^{2}	..	..	9	174	43	..	28	..	..	..	..	5	134	49	..	30	8	..	poi contains ± poi

combinations of svr^{poi} and svr$^{poi\ sq}$ with homozygous bran, an inclination toward the formation of truncated wings. Actually, the slender type is nothing but a beginning of truncation in soft pointed wings; sometimes one wing of slender flies is intermediate to truncated or actually like dumpy (see below). Slender, then, is homozygous bran^{1} with the soft allele of svr^{poi}, bran^{1} homozygous being practically normal. (Consult the table of phenotypes, pp. 388–389.)

The crosses between soft and slender with bran show another phenomenon which must be based upon the soft allele, as it is identical in both crosses. A part of the bran/+, poi s/poi s or bran^{1}/+, poi s/poi s, or bran/bran^{1}, poi s/poi s females and also hemizygous males have a new wing type which we marked as "very slender singed." The wing is still narrower and more indented than is slender, and has near the tip a singed or crumpled-looking spot. This is not a dried-out blister, as the fresh wing shows, but something which might be described as a rudimentary blister. This means that the soft allele acts upon a heterozygous bran, producing almost a blister (the other alleles require a homozygous bran). This, then, is another distinguishing feature of the soft allele. The numbers of singed flies of the constitution bran/+, poi s are rather variable. Usually about one-third of the females and only a few males show the type. Sometimes almost all females and up to one-half males exhibit the type. Probably modifiers are involved. The same singed effect appears also in the heterozygote with bran^{1}, i.e., when soft and slender are crossed, producing bran^{1}/+, poi s flies. We shall meet below with a similar phenotype based upon a different allele.

The cases reported above were not the only ones in which the mutant bran^{1} appeared, visible as slender in the combination with soft (see below). Thus, once after outcrossing soft with bran, F_2 contained, in addition to the expected classes, pointed singed flies (no. 5704) which, inbred, segregated slender but never bran in tests over many generations. The singed flies, therefore, could not have been bran/+, i.e., with the bran crossed into the parents. Tests with bran showed that actually bran^{1} was present, which has no clear homozygous effect without soft. Either bran^{1} had appeared as a mutant, or bran had mutated into bran^{1}.

If soft is combined with homozygous ordinary bran, again the old soft blistered type is found. But it tends to contain a much larger number of truncated blistered flies, up to a short rudimentary wing, than is found in soft blistered involving the other poi alleles + bran. Only a few examples of these and similar crosses are given in table 60. All types reported formerly and in table 60 were further tested in following generations and different backcrosses and found to be of the constitution just assigned to them. A few additional features are visible in the table. As a rule, males tend to show all characters in a lower degree than the females. When females are soft, males may be somewhat like pointed, or even more normal. When singed appears, the males show it in smaller numbers. (Of course, singed and not singed flies of the same class were tested with respect to having the same genetic constitution.)

The table contains also crosses between soft and bran blistered. The latter was homozygous bran^{2} together with the allele svr$^{poi\ sq}$, a combination which shows broad and square wings with a basal blister. All former tests had apparently shown that the bran in bran blist is the normal bran. But the crosses with soft reveal that another allele of bran is involved (as already anticipated above). As early as F_1 some

females and males have wings like slender, with one wing showing a blister at its base; some females, also, have the not blistered wing singed, and one female looks like dumpy and blistered. In F_2 we find ± slender flies, slender singed, slender blistered, soft blistered, and bran blistered, the last-named two classes merging into each other. The expectations are:

Cross +/+; $svr^{poi\ s}/svr^{poi\ s}$ × bran/bran; $svr^{poi\ sq}$
F_1: ♀♀ bran/+, $svr^{poi\ s}/svr^{poi\ sq}$, ♂♂ bran/+, $svr^{poi\ s}$
F_2: ♀♀ : 1 +/+, $svr^{poi\ s}/svr^{poi\ s}$, 1 +/+ $svr^{poi\ sq}/svr^{poi\ s}$, 2 bran/+; $svr^{poi\ s}/svr^{poi\ s}$, 2 bran/+; $svr^{poi\ sq}/svr^{poi\ s}$, 1 bran/bran; $svr^{poi\ s}/svr^{poi\ s}$, 1 bran/bran; $svr^{poi\ sq}/svr^{poi\ s}$
F_2: ♂♂ dto for second chromosome with $svr^{poi\ s}$ and $svr^{poi\ sq}$, respectively.

The new-type slender blistered females in F_2 might be the bran/+ heterozygotes, either with homozygous soft or the compound poi s/poi sq. But the corresponding males must have the soft X, as the combination with square X is known to be pointed. The F_1 males agree with this, but the F_1 females also show the new type. We know, further, that bran/+, $svr^{poi\ s}$ does not show the blistered type; from which it follows that the bran locus which is responsible for the bran blist type with basal blisters is also responsible for the slender blistered type with the same blisters, i.e., the bran is a different one, called $bran^2$. Further generations and backcrosses agree with this.

As table 60 shows, in F_1 soft × bran blist a single female with short, dumpy, blistered wings appeared (6951). Ordinary F_2 from this F_1 (i.e., not from the unusual female) segregated (7094 ff) into slender, poi blist, and sing and soft blistered with transitions to bran blistered. The cross was (+/+, poi s/poi s × $bran^2/bran^2$, poi sq)^2. Therefore in F_2 $bran^2/bran^2$, poi s/poi s segregated as a new combination with the phenotype soft blistered and $bran^2/bran^2$, poi s/poi sq with a phenotype between soft blistered and bran blistered. But the unusual F_1 ♀ dumpy blistered mated to a brother produced in F_2 (7097), a segregation with three-fourths of the individuals as before, but with one-fourth divided into soft blistered and the grandmaternal type. If we make the hypothesis that the new type was based upon a new mutant $bran^{db}$ in conjunction with the pointed allele poi s or poi sq, the cross was $bran^{db}/+$, poi s/poi sq × $bran^2/+$, poi s. This segregated one-fourth $bran^{db}/bran^2$; poi s/poi s or poi s/poi sq ♀♀ and poi s or poi sq ♂♂ one of which was soft blist, the other dumpy blist. As poi sq is known to tend to produce a square or dumpoid phenotype, we assume that the new type was $bran^{db}/bran^2$; poi sq ♂ or poi sq/poi s ♀. The original ♀ must have been heterozygous $bran^{db}/+$, since no bran segregated in F_2, which would mean that $bran^{db}$ is dominant. But it behaved as a recessive in F_2 and in all further crosses, and hence we must assume that the dominance in the first female, arisen by mutation, was an accidental feature. From extracted "dumpy blistered" from the F_2 7097 a true breeding stock was established which in further tests turned out to be homozygous $bran^{db}/bran^{db}$, poi sq/poi sq. Immediately after isolation of this stock, the dumpy blistered flies were tested against second-chromosome markers, with the result that the two original right ends of the second chromosomes were needed for the phenotype. A backcross with bran blistered resulted in a nonclassifiable series of phenotypes from dp blist to bran blist, which is expected from the backcross $bran^{db}/bran^2$; poi s/poi sq × $bran^2/bran^2$, poi sq. Another

test backcross of dp blist × soft blist F_1 with soft blist = $bran^{db}/bran^{2}$; poi s/poi sq × bran/bran, poi gave the expected segregation into dumpy blist and soft blistered. The decisive test was made after the stock had become homozygous by breeding from typical dumpy blistered, i.e., $bran^{db}/bran^{db}$, poi sq/poi sq selected from $bran^{db}/bran^{2}$; poi s/poi sq inbred, (stock 7960 dp bl). Females of this homozygous stock × bran ♂ produced in F_1 all ♀♀ bran, all ♂♂ pale soft folded. The latter were a very characteristic new type. The wings are long and soft and blistered when hatching and later fold lengthwise into a wing looking like a wet towel. The paleness of the silver type is more extreme than usual. The ♀♀ bran are $bran^{db}/bran$, and the folded ♂♂ are $bran^{db}/bran$, poi sq. F_2 shows a very characteristic segregation into 3 ♀ and ♂ of the same pale soft folded type, including also soft blist, 4 ♀ and ♂ bran, and less than 1 (⅛) dumpy blistered (lower vitality). The segregation was clearly:

Cross: $bran^{db}/bran$, poi sq/+ × $bran^{db}/bran$, poi sq
F_2: ♀♀ 1: $bran^{db}/bran^{db}$, poi sq/poi sq = 1 dumpy blistered
2: $bran^{db}/bran^{db}$, poi sq/+ = 1 bran
3 and 4: $bran^{db}/bran$, poi sq/poi sq = 2 soft folded blistered
5 and 6: $bran^{db}/bran$; poi sq/+ = 2 bran
7: bran/bran, poi sq/poi sq = 1 soft blistered–dp blistered
8: bran/bran; poi sq/+ = 1 bran

The F_2 types were tested in F_3 and by outcrossing to parent stock. The constitution was confirmed, but it turned out that homozygous dp blist had a tendency toward the heterozygous soft blistered folded phenotype, possibly caused by external conditions.

The different phenotypes thus obtained are tabulated below (pp. 388 f.). Clearly, $bran^{db}$ alone has the phenotype bran, but in combination with poi sq, dumpy blistered. The effect is somewhat dominant in compounds, but not in the heterozygote, though the first mutant female had shown dominance in the heterozygote.

Still another combination can be made by crossing poi blist = bran/bran; $svr^{poi\ bl}$ with bran blist = $bran^{2}/bran^{2}$, $svr^{poi\ sq}$. The reciprocal F_1 males are somewhat different. F_1 poi bl × bran bl, i.e., ♂ $bran/bran^{2}$, $svr^{poi\ bl}$, are still blistered, more pointed, and only a few have short wings. The reciprocal cross with ♂♂ $bran/bran^{2}$, $svr^{poi\ sq}$ does not show blistering in all individuals, which is clearly an influence of the svr allele; but many males possess short wings (like rudimentary). In both reciprocal F_2 one-eighth of the males have the rudimentary type, which then must be the combination bran/bran, $svr^{poi\ sq}$ or $bran^{2}/bran^{2}$, $svr^{poi\ bl}$.

As the X chromosomes of the first found allele poi s which was used for the further checks had been derived either from wild type or bs stocks (or both), one might not expect the presence of the different translocations and transpositions presumably derived from px bl (though $svr^{poi\ h}$ was derived also from wild type!). If they were present, it would mean that the mutation to the soft allele was somehow linked up with these other changes, as it had also to be assumed for $svr^{poi\ h}$. Therefore the sex ratios of outcrosses involving both poi alleles were checked. They are as shown in table 61, both for soft derived from a px bl X, and for soft in slender derived from a foreign X.

Table 61 shows a definite rule: High ratios for slender, either near 4 : 3 or 2 : 1, are always present when the father introduces a not sl X chromosome and the

mother is homozygous or heterozygous for sl, i.e., all crosses (sl × N) × N, sl × (N × sl). Normal sex ratios obtain whenever the father is slender. This looks as if one-half of both ♀♀ and ♂♂ homo- or hemizygous slender were lethal in the presence of homo-

TABLE 61

Sex Ratios involving svr$^{poi\,s}$

Cross	♀	♂	Ratio
slender (sl) inbred	614	518	1.18
RF_2 sl × (+ × sl)	751	560	1.32
RF_2 sl × (sl × +)	430	393	1.09
RF_2 (sl × +) × sl	652	611	1.07
RF_2 (+ × sl) × sl	434	429	1.01
RF_2 $\underline{Y}$ × ($\underline{Y}$ × sl)	881	838	1.05
RF_2 (sl × Xple) × Xple	241	132	1.83
RF_2 sl × (SD × sl)	145	74	2.0
F_1 sl × bran	81	42	2.0
F_1 sl × a px sp	45	25	1.8
F_1 sl × soft	68	53	1.3
F_1 soft × bran	324	189	1.71
F_1 soft × bran blist	31	28	1.1
F_2 (soft × bran)^2	159	175	0.9
F_2 (soft × bran blist)^2	404	318	1.27
F_2 (sl × bran)^2	185	154	1.2
RF_2 (sl × a px sp) × a px sp	92	69	1.32

zygous autosomes, just as was noted for the other poi alleles. (This does not hold for bran, which is not foreign!) A check with marked second chromosomes actually reveals the same situation as was found for poi: most males homozygous for a for-

TABLE 62

sl Backcrosses with ll sp and a px sp

(bran in slender remains heterozygous and is therefore without influence)

Cross	♀				♂					
	+	ll sp	ll	sp	+	ll sp	ll (sp) sl	sp	ll	sl
1. (ll sp × sl) × sp	320	243	1	2	192	116	..	2	..	95
Expect	1	1	c.o.	c.o.	1	1	1	c.o.	c.o.	1
	+	a px sp	a px	sp	+	a px sp	a px (sp), sl	a px	sp	sl
2. (sl × a px sp) × a px sp	48	41	2	1	26	25	4	2	..	12

Sex ratio: (1) 1.4; (2) 1.33.

eign second chromosome are lethal (table 62). The result is exactly as with the pointed alleles. Soft suppresses sp. In the first cross the group ll (sp) sl can therefore hardly be distinguished (except for the pale color). This combination is almost lethal but for a few survivors, visible in the second cross. Moreover, the slender class is deficient. We point to the discussion of the parallel facts for pointed. Also, the

transposition in the X chromosome was tested, though only on a small scale, with results paralleling those for pointed. All these facts are of importance for the discussion of the origin of these mutants.

Finally, the standard translocation test, which in some alleles showed a suppressor action with eyeless, is presented in table 63. The females show clearly the suppressor action as seen when plus and ey, e and e ey, bw and bw ey are added (see also table 55). But in the males this is not the case, suggesting that the interaction between autosomes and the X chromosome is not a simple one (see discussion above, p. 359).

The alleles bran^{dp} (bran dumpy) and bran^{r} (bran rudimentary).—The very remarkable allele bran^{dp} has appeared repeatedly. As it has no visible effect except in combination with one of the svr^{poi} alleles, it was recognized only where the latter was present. The combination of bran^{dp} with poi has a highly variable effect. The majority of the individuals resemble pointed; a certain percentage have one pointed and

TABLE 63

Patt × (Patt × slender)

♀								♂							
Patt	bw e	bw ey	e ey	bw	e	ey	+	bw ey	bw e	bw ey	e ey	bw	e	ey	+
91	102	57	95	172	123	76	165	90	44	117	77	129	79	111	191

one dumpy (truncated) wing; some have one dumpy wing and one with all transitions from pointed to dumpy, and another group have both wings truncated; further variants depend upon the respective poi allele, as will be described below. (See text fig. 2.) Thus, bran^{dp} can only be discovered as flies with one wing poi, one truncated (abbreviated henceforth poi: dp), or both truncated in an otherwise pointed culture. As such, they were repeatedly found in svr^{poi} stock as single flies and also in crosses with this stock. The following are some of the exactly known pedigrees.

1. We reported above on one of the crosses of pointed blistered × Bld T (3922) which produced in F_1 pointed males and Bld females, all looking like Bld(1)Df. F_2 (4539) produced both Bld females and males of this type. It turned out that a dominant Bran allele had arisen which, heterozygous with Bld, produced these Minute-like blond broad-winged flies (see above, p. 363). From this F_2 the segregating poi blist flies (= bran/bran, poi^{bl}) were extracted. Their offspring (F_3 4713) consisted of only 25 ♀ 6 ♂ poi blist, 1 ♀ 1 ♂ + and 1 ♀ truncated and blistered. As rudimentary was one of the mutants derived before, this ♀ dp blist was crossed to a male containing both pointed and rudimentary in the X chromosome. All offspring (no. 5,000) were pointed as expected, but 1 ♀ was poi : dp. We remember that the great-grandparents had contained dominant Bran, which in the presence of poi produces soft blistered flies. The offspring of this F_3 may then contain rudimentary, pointed and soft blistered, and in addition poi : dp or dumpy (dp not meaning the locus dp, but only the phenotype of this description) if it is inherited. The following generations up to the establishment of the stock called pointed dumpy (poi : dp), being the new bran^{dp} + poi, are recorded in table 64 (note that r contains poi but is epistatic).

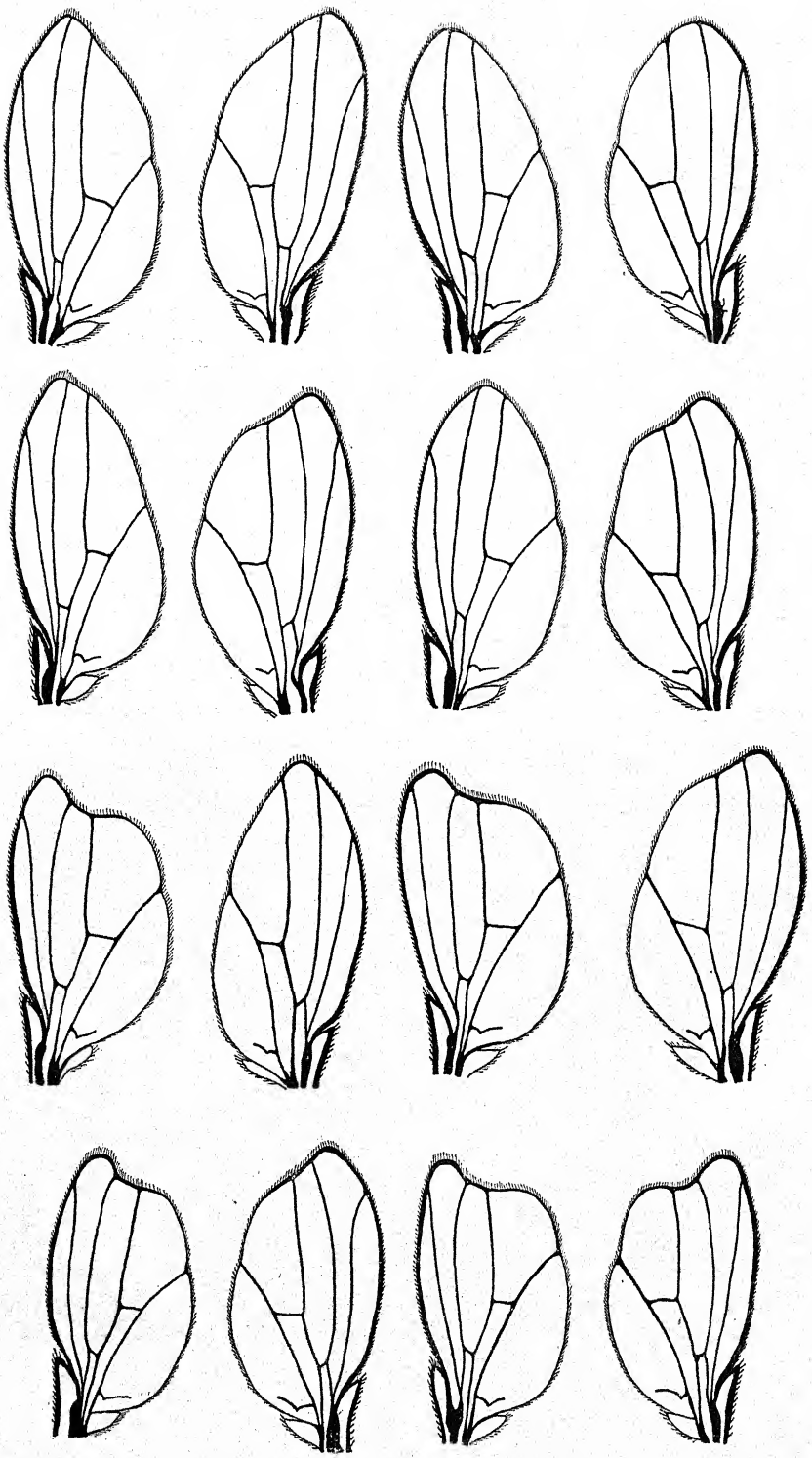


Fig. 2. Series of wing phenotypes of poi : dp. The beginning, both wings pointed, omitted. Both wings of one fly are always drawn.

TABLE 64

PEDIGREE OF poi:dp AFTER F_3 5000

No.	Cross	♀ poi	♀ poi:dp	♀ dp	♀ soft bl	♀ rud	♀ N-Df	♀ dp bl	♂ poi	♂ poi:dp	♂ dp	♂ soft bl	♂ rud	♂ dp bl	Remarks
5101	F_4 5000² ♀ poi:dp..	45	8	13	8	..	..	..	21	..	..	..	15	..	
5102	F_4 5000² ♀ poi.....	53	7	5	12	..	..	..	19	..	..	11	22	..	
5103	F_4 5000² ♀ poi.....	66	1	5	16	..	..	..	35	..	..	15	38	..	
5166	F_5 5101² poi:dp × poi.....	54	3	13	14	..	..	..	19	2	12	12	14	..	
5171	F_5 5101² soft bl × r	12	1	9	8	..	..	..	14	..	..	24	..	..	
5172	F_5 5101² poi × r...	43	2	..	19	39	..	..	27	..	..	11	22	..	rud. contains also dp, cannot be classified
5208	F_6 5166² poi × dp..	56	3	2	..	..	..	..	32	..	..	..	..	..	
5209	F_6 5166² poi × soft bl.....	19	..	..	11	8	..	..	8	..	..	7	16	..	
5294	F_7 5208² poi:dp × poi.....	64	21	5	..	..	..	..	33	..	..	..	23	..	1 gynander ♀ poi ♂ dp
5337	F_8 5294² poi:dp × poi.....	46	3	4	..	..	..	..	48	..	6	..	..	..	10 ♂ dwarf
5328	F_8 5294² poi × rud.	44	..	..	..	19	..	..	38	..	..	..	22	..	
5329	F_8 5294² poi × poi.	76	..	..	..	..	2	..	50	..	..	..	..	..	1 ♂ bl 2 ♂ dwarf
5357	F_9 5329² N ♀ ♂ ?..	114	6	7	..	..	54	..	55	..	..	..	..	..	
5373	F_{10} 5357² ♀ poi....	57	6	6	..	..	..	..	55	4	..	..	..	..	
5374	F_{10} 5357².....	75	4	..	..	..	..	..	87	..	..	..	..	..	
5375	F_{10} 5357² ♀ N-Df..	34	1	1	..	..	27	..	34	1	..	..	..	..	Some N ♀ show dp
5376	F_{10} 5357² ♀ N-Df..	34	1	1	..	..	47	..	33	..	..	..	..	..	Some N ♀ show dp
5378	F_{10} 5357² ♀ dp....	55	12	4	..	24	..	24	59	1	..	10	..	..	24 ♀ are rud bl
5390	F_{11} 5373² poi:dp...	60	8	13	..	..	..	..	55	7	..	3	..	2	Stock poi:dp
5391	F_{11} 5373² dp × poi:dp.....	30	8	12	..	..	..	8	25	4	1	..	..	4	
5393	F_{11} 5378² rud bl × soft bl.....	..	..	..	..	All	..	..	..	..	..	All	..	..	♀ most rud bl, few soft bl; ♂ most soft bl, few rud bl

The table shows how the poi : dp stock with its typical variation poi→poi : dp→ dp→dp blist was extracted from the offspring of the original poi : dp flies. There is nothing unexpected otherwise. The rudimentary X chromosome was again selected out. As there is a very high percentage of crossing over between svr^{poi} and r introduced into the same chromosome, it cannot be decided whether finally the allele svr^{poi} or $svr^{poi\ bl}$ went into the poi : dp stock. The dominant Bran originally present was also selected out. It produces in different combinations with poi alleles rudimentary blistered and soft blistered phenotypes as selected in no. 5393. This is important, because as we shall later see, the stock poi : dp sometimes contains ordinary bran. This must be the result of mutation after the stock was isolated. The new mutant Notch Deficiency (since 5329 F_8) can show pointed, poi : dp, and dp phenotypes and is therefore independent of the poi : dp genotype.

TABLE 65

PHENOTYPE OF BROODS FROM PAIRS FROM poi:dp STOCK

No.	Parental phenotype	♀				♂			
		poi	poi:dp	dp	dp bl	poi	poi:dp	dp	dp bl
I	poi × poi	19	4	1	..	12	..	3	..
II	dp × dp	15	6	16	..	15	6	11	..
III	dp × dp	71	20	13	8	73	4	10	4
IV	dp × dp	35	15	31	9	53	2	4	10
7113	poi:dp × poi:dp	2	11	6	..	15	1	..	..

2. Thirty F_2 crosses of $svr^{poi} \times svr^{poi\ h}$ were bred. Among the 6,000-odd flies were 2 ♀ with dp wings. Only one gave offspring which were normal, as were two more generations. Again, in one F_3 from dwarfed F_2 parents 1 ♀ poi : dp among 14 ♀ was found. She produced only 6 daughters, 1 again poi : dp, which was sterile.

3. In a pointed stock containing a bobbed allele which produces etching of the abdominal tergites (see below, p. 390), called poi achi 6317, two females poi : dp (also achi) were found. They were sterile. Simultaneously, one male with scalloped wings appeared which turned out to be a Beadex allele. This ♂ mated to a poi achi sister produced only 3 daughters, 1 ♀ poi bb achi, 1 ♀ dp bb achi, 1 ♀ bb achi with a new type of wing. The dumpy-like ♀ crossed with the poi : dp stock produced no poi : dp in F_1 or F_2, but soft blistered in F_2. In later generations the dumpy blistered, rudimentary blistered, and soft blistered flies segregated together. This prevents a decision on the composition of the original dumpy ♀ which might have contained $bran^{dp}$ or bran.

4. We shall report below that poi : dp has also been produced by X-raying and, in addition, that single individuals have cropped up in different crosses so frequently that they were not tested any more.

The phenotype.—The stock poi : dp always contains a majority of pointed flies and a minority of poi : dp and dp phenotypes. But in breeding from pairs rather constant ratios are obtained, as table 65 shows. As a rule the largest class has pointed wings. Flies with one wing pointed and the other like dumpy, and flies with both wings truncated, of equal or unequal length (all transitions), occur in about equal numbers, and in large broods—they are usually small—dumpy phenotypes

with a blister in one or both wings are sometimes found (see below, allele bran^r). Females and males contain the same types, but the aberrant type has a lower expressivity in males (as most of the wing types studied in this paper do), visible as a lower percentage of the not pointed types. (All flies are pale, being homozygous svr alleles.)

Frequent selections of the types were made. One experiment over a few generations is presented in table 66. In the first sections of the table, pointed flies were

TABLE 66

SELECTION FOR pointed IN poi:dp, ALWAYS TWO BROODS ADDED

Generation	♀ phenotype				♂ phenotype			
	poi	poi:dp	dp	dp blist	poi	poi:dp	dp	dp blist
1	68	12	6	..	65	2	..	..
2	91	3	1	..	65	..	..	..
3	79	20	13	4	105	3	..	..
4	76	4	..	1	105	4	..	..
5	47	2	..	..	32	..	..	..
SELECTION FOR THE PHENOTYPE poi:dp								
	♀				♂			
1	28	3	5	..	30	5	1	..
2	29	..	..	1	36	1	..	..
3	30	1	4	2	32	2	..	2
4	28	5	10	2	29	4	6	..
5	24	3	4	1	26	3	3	..
SELECTION OF dp FROM STOCK								
	♀				♂			
	35	3	..	..	29	..	..	..
	21	1	..	..	26	..	..	..

selected from the poi : dp stock and each subsequent generation. One might say that a little effect was observed, probably by selection of modifiers, though the variation in consecutive generations does not seem to show a definite trend. In the same way, poi : dp was selected without any visible effect. Neither did dumpy selected from stock increase its share. But the few dp blist individuals coming out occasionally and also found in the stock always bred true (see below). As it appeared that relatively more truncated flies appear in mass cultures, probably external conditions are also involved. It did not seem worth while to follow up this subject.

Genetics.—All tests for the pointed allele in poi : dp show that it is the ordinary svr^{poi} (see discussion of origin) and that it is always present in homozygous condition in all the phenotypes described. Also, the other features of the svr^{poi} stock are found as seen in the sex ratios of crosses, which thus do not need further discussion. A standard test with dominant markers revealed that poi : dp (*all phenotypes*) requires the simultaneous presence of svr^{poi} homo- or hemizygous and something in

the second chromosome of the poi : dp stock, also in homozygous condition, as table 67 shows.

The father was heterozygous for all autosomes and had the poi X chromosome. Flies heterozygous for S (or SD) introduced by the father without crossing over were all pointed ; flies without S, i.e., homozygous for the second chromosome from poi : dp, showed the typical series from poi to poi : dp, dp, and dp blist in both sexes whether D was present or not.

This result suggested an interaction with a bran allele, especially after the reciprocal cross with crossing over showed a location of the second chromosome locus far from Star. All other tests, such as $\underline{y} \times$ poi : dp, and following generations or crosses with recessive markers agreed that the variable poi : dp types were the product of collaboration between svr^{poi} and a homozygous second-chromosome locus.

TABLE 67

♀ 5390 poi:dp × ($\underline{y}$, S/+, D/+ × poi:dp)

Phenotype ♀									
S	S, D	D, poi	D, poi:dp	D, dp	D, dp bl	poi	poi:dp	dp	dp bl
38	68	34	2	10	12	21	1	12	12
Phenotype ♂									
S	S, D	D, poi	D, poi:dp	D, dp	D, dp bl	poi	poi:dp	dp	dp bl
44	51	35	1	5	10	19	3	1	11

When the second chromosome was tested for bran, it turned out that the poi : dp stock contained in an irregular way another bran allele with phenotypical bran effect which, however, has nothing to do with the poi : dp phenotypes—a fact which led to much confusion until analyzed. The majority of crosses poi : dp (all types except that which was called above dp blist) × bran produce normal daughters and pointed sons. Anticipating that poi : dp contains an allele $bran^{dp}$, this means that the combination ♀ $bran^{dp}$/bran, svr^{poi}/plus is normal and the ♂ with the same bran compound and svr^{poi} is pointed, i.e., $bran^{dp}$ acts like wild type. But in about one-fourth of such crosses F_1 females are half normal half bran, and the majority of males pointed, a minority soft blistered, or rudimentary-like and blistered. Soft blistered, when tested, turned out to be the ordinary bran/bran, svr^{poi} combination except for a tendency toward dumpy blistered and the rud blist (= phenotype rudimentary blistered) types. The mother, therefore, had been heterozygous for bran or an allele which, as stated above, must have originated as a mutant in the poi : dp stock after its isolation and spread through the stock. If this is true, occasional matings of heterozygous bran flies must occur in the stock, resulting in ¼ soft blistered and rud blist offspring. As this type has a lower viability, it cannot hold its own and will remain rare. Actually, occasional soft blistered or rudimentary blistered (phenotype, not locus r !) flies appear in the poi : dp stock. Their analysis shows that they are homozygous for a bran allele, different from $bran^{dp}$, and, in addition, for pointed. The frequency, sometimes preponderance, of the rudimentary blistered type in this combination (which is rare in ordinary soft blist) indicates

that another allele than bran is involved, which we shall call bran^r. This has turned out to be true, as the compounds and combinations show: bran/bran = broad round, bran^{dp}/bran^{dp} = +, bran^{dp}/bran^r = broad round tendency to dumpy, bran/bran; poi = soft blistered, bran^{dp}/bran^{dp}; poi = pointed to poi: dp to dp; bran^{dp}/bran^r; poi = pointed, bran^{dp}/bran^r; poi = the poi: dp series, bran^r/bran^r; poi= rud blist–soft blist (more rud blist) bran^r/bran; poi = rud blist–soft blist (more soft blist).

We have already seen in the selection experiments (see p. 377) that the type dp blist (varying into rud and soft blist) sometimes segregated from poi: dp and, if

TABLE 68

F$_1$ Crosses with Different Types from poi:dp Stock

No.	Type of poi:dp parent	Other parent	F$_1$ ♀	F$_1$ ♂	
I	poi:dp ♀	bran	+	poi	A later repetition with 10 pairs gave three times, this result; seven times, result like IV
II	dp ♀	bran	+	poi	Sex ratio, 2 : 1
III	poi ♀	bran	+	poi	Sex ratio, 2 : 1
V	poi ♀	bran	+	poi	Sex ratio, 2 : 1
VI	dp ♀	bran	+	poi	Sex ratio, 2 : 1
IX etc.	poi:dp ♀	+	+	poi	Fathers of different crosses are + or marked stocks
IV	dp ♀	bran	½ + ½ bran	poi and soft blist	♂ rud blist and soft blist poorly viable, less than ½
VII	dp ♀	bran	½ + ½ bran	poi and soft blist	As above. Sex ratio, 6.5 : 1 (♀ 35 + 30) bran ♂ 8 poi 2 soft blist
VIII	poi:dp ♀	poi	poi	poi	
XXV	poi:dp ♂	y ♀	y	poi	
7202	poi ♂	bran ♀	+	+	
7203	dp ♂	bran ♀	½ + ½ bran	½ + ½ bran	

extracted, bred true. This was bran^r/bran^r, poi. The numbers were always far below the expected ¼, owing to lower viability. Also the extracted line contained a rather small number of flies. Most of the data are self-explanatory and show the correctness of the formulations. The tables show, further, that in the first series made (table 68) the poi : dp phenotype did not contain bran^r, but that the dp type did. In a later check (table 68, I, note) both conditions were found among 10 poi : dp types which were tested. The bran^r combinations were frequently less viable. In one case (table 70, note d) it seems that bran^r had just arisen as a mutation. In table 71 we analyzed the soft blist and rud blist types found occasionally in poi : dp stock as the combination dp bl–soft bl, i.e., bran^r/bran^r, poi. The results of the analysis agree with the expectations derived from the formulas. The low viability of this combination is also apparent.

Tables 68–71 contain some of the data from which the foregoing statements were derived.

An interesting check upon the analysis is derived from crosses with bran blistered stock which exhibits the phenotype of broad square wings with a basal blister based

upon the genotype bran^2/bran^2, poi^{sq}. A series of crosses between poi : dp and bran blist gave different F_1 results, depending upon the presence or absence of bran^r, just as was the case with poi : dp × bran. Table 72 contains the data arranged in genetical groups.

The cross is supposed to be: bran^{dp}/bran^{dp}, poi/poi × bran^2/bran^2, poi^{sq}. All daughters are bran^{dp}/bran^2, poi/poi^{sq}; all sons, bran^{dp}/bran^2, poi. The result is almost like that from inbreeding poi : dp, except that the percentage of poi : dp

TABLE 69

SOME F_2 FROM CROSSES OF TABLE 68

No.	Cross	♀					
		+	poi	poi:dp	dp	bran	osft bl
I	(poi:dp × bran) I × bran	50	..	..	..	38	..
II	(poi:dp × bran) I × poi:dp	38	20	1	..	11	5
7699	(poi × bran)^2	11	13	..	..	2	1
7410	(bran × poi)^2 7202^2 (ratio)	3	..	..	..	1	..
7411	7203^2 (bran × dp)^2 F_1 + (ratio)	3	..	..	..	1	..
7430–31	(y × 7045 poi:dp)^2	All	..	..	..	..	..
7432	(y × 7044 soft bl)^2 (ratio)	3 y	..	..	..	1 y	..
VII	(poi:dp × +) × +	85	..	..	..	..	..
V	(poi:dp × +) × poi:dp	35	19	2	10	..	..

No.	Cross	♂					
		+	poi	poi:dp	dp	bran	soft bl
I	(poi:dp × bran) I × bran	29	44	..	..	23	..
II	(poi:dp × bran) I × poi:dp	27	25	..	1	15	..
7699	(poi[a] × bran)^2	15	7	..	..	3	3
7410	(bran × poi)^2 7202^2 (ratio)	3	3	..	..	1	1
7411	7203^2 (bran × dp)^2 F_1 + (ratio)	3	3	..	..	1	1
7430–31	(y × 7045 poi:dp)^2	All	..	..	..	..	..
7432	(y × 7044 soft bl)^2 (ratio)	..	3	..	..	..	1
VII	(poi:dp × +) × +	45	29	..	..	..	..
V	(poi:dp × +) × poi:dp	22	20	1	..	..	..

[a] poi = phenotype in poi:dp stock.

and dp flies is much smaller, and almost nil in the males. This shows that bran^{dp} and bran^2 are much more similar than are bran^{dp} and bran, and the compound action more or less intermediate. Actually, both tend to produce a truncated wing. As the former data indicate, the second group clearly had a mother heterozygous for bran^{dp}/bran^r. The cross thus was bran^{dp}/bran^r; poi/poi × bran^2/bran^2; poi^{sq}, resulting in

1) ½ ♀ bran^{dp}/bran^2 poi/poi^{sq}
2) ½ ♀ bran^r/bran^2 poi/poi^{sq}
3) ½ ♂ ditto with poi
4) ½ ♂ ditto with poi

Actually the ♀♀ and ♂♂ nos. 1 and 3 are the same as in the former group. i.e., pointed, with a small percentage of poi : dp and dp. The ♀♀ of no. 2 ought to be between dumpy (the bran^r type) and bran blist. Actually, the majority are dumpy, varying into a type of dumpy blistered and bran blistered. The males have the poi

TABLE 70

RF_2 AND F_2 FROM CROSSES F_1 poi:dp × bran Nos. 1–10 REPORTED IN NOTE TO No. 1, TABLE 68 (F_1 not segregating bran and soft blist, i.e., without bran^r in poi:dp, is called normal, the others "segr.")

Cross	♀					
	F_1	+	poi	bran	poi:dp types	dp blist–soft blist
1^2 + × poi	norm.	42	38	7	..	..
10^2 + × poi	segr.	41	157[a]	6	..	2
9^2 + × soft bl	[b]	2	..	1	..	1
10^2 + × soft bl	segr.	2	..	1	..	1
		ratio		ratio		ratio
soft bl stock × soft bl no. 5	segr.	..	..	..	..	All
bran stock × soft bl from 9	segr.	..	..	All	..	..
bran stock × poi 9	[b]	½	..	½	..	..
soft bl stock × poi no. 1	norm.	..	½	..	..	½
♀ bran 10 × bran stock	segr.	..	..	All	..	..
poi:dp stock × soft bl 5	segr.	..	23[d]	..	9	..
poi:dp stock × soft bl 6	segr.	..	13[d]	..	8	10

Cross	♂				
	+	poi	bran	poi:dp types	± soft bl
1^2 + × poi	20	16	5	..	..
10^2 + × poi	16	26	14	..	..
9^2 + × soft bl	15	2	14	..	9
10^2 + × soft bl	2[c]	..	1	..	1
	ratio		ratio		ratio
soft bl stock × soft bl no. 5	..	..	..	..	All
bran stock × soft bl from 9	..	..	All	..	..
bran stock × poi 9	½	..	½	..	..
soft bl stock × poi no. 1	..	½	..	..	½
♀ bran 10 × bran stock	..	..	½	..	½
poi:dp stock × soft bl 5	..	30	..	5	..
poi:dp stock × soft bl 6	..	16	..	4	13

[a] 1 ♀ new mutant (vortex).
[b] F_1 contained 109 ♀ +, 57 ♂ poi, 1 ♀ bran, 3 ♂ soft blist, i.e., 4 eggs out of 170 contained bran^r, which looks like mutation.
[c] Considerable dominance of bran.
[d] 1 ♀ singed.

X chromosome which with bran^2 produces soft blistered, and therefore with the compound all transitions from dp blist to soft blist.

In one instance a strange result was obtained: all females were dumpy or dumpy blistered, all males dp blist or soft blist, with all transitions. The females were backcrossed both to bran blist and to poi: dp. The backcross (poi × bran bl) ♀ dp × bran blist gave:

14 ♀♀ dp, 9 dp bl, 14 ± soft bl (bran bl), 5 folded
1 ♂ dp, 4 dp bl, 40 bran bl–soft bl, 1 ♂ pointed singed

Comparing this with the results of the former group, it follows that the mother had been homozygous for bran^r but exhibited phenotypically poi: dp instead of rudimentary blistered.

TABLE 71

Soft bl FROM poi:dp STOCK

No.	Cross	♀ poi	♀ poi:dp	♀ dp	♀ dp bl	♀ soft bl	Remarks
7001	♀♂ poi:dp from F_1 soft bl × poi	17	9	11	3	5	
7043	♀♂ poi from F_1 soft bl × poi	12	10	14	..	10	
7044	♀♂ dp from F_1 soft bl × poi	16	11	10	1	6	
	Σ	45	30	35	4	21	
7048	rud bl ♀, soft bl ♂ from poi:dp stock	..	1	1	..	All	Many rud bl
7198	7701[2] poi:dp × poi	10	2	11	..	4	Mut. N-def.
7199	7701[2] poi:dp × poi	22	5	6	..	8	
7200	7701[2] ♀♂ poi	16	2	2	..	..	
7217	7701[2] ♀♂ poi:dp	26	4	2	..	..	
7227	7701[2] ♀♂ poi	5	7	7	..	2	
7228	7701[2] poi:dp × dp bl	..	4	7	..	3	
7249	7043[2] soft bl	..	..	..	..	All	Only few rud bl
7218	7048[2] rud bl						
7219	7048[2] rud bl × soft bl	..	..	..	..	All	Only few rud bl
7223/24	7048 soft bl × stock soft bl and rec.	..	..	..	..	All	Part rud bl
7236	7044 rud bl ♂ × ♀ soft bl stock	..	..	..	..	21	10 rud bl
7260	7043 poi:dp × bran	..	..	..	1	..	29 +, 23 bran
7439	7218[2] rud bl	..	..	..	..	All	Most rud bl
7442	7227[2] poi:dp	15	3	12	..	..	
7443	7227[2] dp × poi:dp	10	3	7	..	..	

No.	Cross	♂ poi	♂ poi:dp	♂ dp	♂ dp bl	♂ soft bl	Remarks
7001	♀♂ poi:dp from F_1 soft bl × poi	27	8	3	6	5	
7043	♀♂ poi ditto	30	2	..	..	2	
7044	♀♂ dp ditto	17	..	1	1	5	
	Σ	74	10	4	7	12	
7048	rud bl ♀, soft bl ♂ from poi:dp stock	..	..	..	..	All	Most soft bl
7198	7701[2] poi:dp × poi	5	2	..	..	3	
7199	7701[2]	30	..	..	..	3	
7200	7701[2] ♀♂ poi	19	..	..	..	..	
7217	7701[2] ♀♂ poi:dp	13	1	1	..	..	
7227	7701[2] ♀♂ poi	12	6	2	..	2	
7228	7701[2] poi:dp × dp bl	5	1	1	7	7	
7249	7043[2] soft bl	..	..	..	..	All	Only few rud bl
7218	7048[2] rud bl						
7219	7048[2] rud bl × soft bl	..	..	..	..	All	Only few rud bl
7223/24	7048 soft bl × stock soft bl and rec.	..	..	..	..	All	
7236	7044 rud bl ♂ × ♀ soft bl stock	..	..	..	..	13	1 rud bl
7260	7043 poi:dp × bran	7	..	..	..	6	
7439	7218[2] rud bl	..	..	..	..	All	Most rud bl
7442	7227[2] poi:dp	12	1	..	..	..	
7443	7227[2] dp × poi:dp	14	1	1	..	..	

If there was no error in recording, no explanation can be offered. The backcross (poi : dp × bran bl) ♀ dp × poi : dp produced:

13 ♀♀ poi, 9 poi : dp, 11 dp, 2 dp bl, 14 ± soft blist
25 ♂♂ poi, 7 poi : dp, 7 dp, 11 ± soft blist

This is the expected result from the cross $bran^{r}/bran^{2}$, $poi/poi^{sq} \times bran^{dp}/bran^{dp}$, poi under the same assumption regarding the grandmother as before (see table of phenotypes, p. 388).

Also, the first two groups of table 71 were tested in further generations and backcrosses as well as with testers like bran and soft blistered. The results were those expected from the foregoing data: poi:dp and bran blist could be extracted. In F_2 (bran^{dp}/bran^{s}, poi/poi^{sq} × ♂ ditto poi)^2 the combination bran^{dp}/bran^{dp}, poi^{sq} could be obtained as a novelty, and in F_2 (bran^{dp}/bran^{r}, poi/poi^{sq} × ditto ♂ poi)^2

TABLE 72

F_1 poi:dp × bran blist

Mother (phenotype)	♀				♂				Remarks
	poi	poi:dp	dp	± soft bl	poi	poi:dp	dp	± soft bl	
5 times poi:dp. 4 times poi....	296	14	22	..	237	1	1	..	1 ♀♂ poi ll 1 ♂ like soft bl (sterile)
5 times poi:dp.	90	3	61	20	71	1	3	49	♀ soft bl = ± bran bl ♂ soft bl = ± soft bl
Once poi:dp...	..	..	All	..	..	..	..	All	♀ dp and dp bl like bran bl ♂ dp bl and soft bl

the novelties bran^{r}/bran^{r}, poi^{sq} and bran^{dp}/bran^{dp}, poi^{sq} would segregate. In the first F_2 the expectation is (see table of phenotypes below, table 74);

♀ 6 poi dumpy (= poi⟶poi : dp⟶dp, most poi), 2 ± soft blist
♂ 5 ditto (most poi), 1 bran blist, 1 ± soft blist, 1 novelty bran^{dp}/bran^{dp}, poi^{sq}

In the second F_2 the expectation is:

♀ 6 poi dumpy (most poi), 2 rud bl–soft blist
♂ 3 poi dumpy, 1 rud bl–soft bl, 2 nov. bran^{dp}/bran^{r}, poi^{sq}, 1 nov. bran^{r}/bran^{r}, poi^{sq}, 1 nov. bran^{dp}/bran^{dp}, poi^{sq}

The segregation in the first case is shown in table 73. The ratios are not relevant,

TABLE 73

(poi:dp × bran bl)^2

	No. 7730	poi	poi:dp	All trans. dp–bran or rud bl
♀	7712 ff.....	94	14	74
♂	7712 ff.....	119	7	74

since the type dumpy belonging to the poi:dp range of variation is contained in the class with all transitions between dumpy, dumpy blistered, bran blist, and rud blist. This makes it difficult to ascribe a definite type to the combination bran^{dp}/bran^{dp}, poi^{sq}, but a few selection experiments point to a phenotype like dumpy blistered. We did not follow this up. The second type of F_2 was still more difficult to analyze. We had only one F_2 which was clearly in this category. Here the number of transitions between dumpy and soft blistered was very high, and the new combination bran^{r}/bran^{r}, poi^{sq} must have been in this group. Since in this case a majority of soft blistered types appeared, this is probably the phenotype of the combination.

It did not seem worth while to continue this analysis. Only a few combinations of poi : dp with slender, i.e., $bran^1/bran^1$, poi^s, were made. F_1 poi : dp × slender was slender in both sexes, with some singed flies, as is typical for slender crosses. Pointed dumpy crossed with soft (poi^s) is pointed, with a few singed individuals. Thus $bran^{dp}/+$ reacts with poi^s, as do the other bran alleles. By backcrossing to bran blist, ♀♀ $bran^{dp}/bran^2$, poi^s/poi may be obtained. Some of these are poi : dp and singed. The ♀♀ and ♂♂ $bran^1/bran^2$; poi^{sq}/poi^s or poi are soft blist; a few are like bran blist (see table of phenotypes, table 74).

Pointed dumpy was assumed to be the product of $bran^{dp}$ homozygous with svr^{poi}. To make sure that actually the ordinary svr^{poi} and no other allele or sex-linked modifier was involved, a svr^{poi} combined with white, i.e., practically the entire X chromosome right of svr^{poi}, replaced and marked with w, which is closely linked with svr^{poi}, was crossed to poi : dp. In F_2 the poi : dp types appeared both with poi and with w poi.

Finally, another peculiarity of the allele $bran^{dp}$ must be mentioned. In crosses involving the locus ebony the heterozygote shows a dominance effect of ebony. We stated above that pointed itself tends to make ebony a little dominant (a trident visible). But the effect under discussion is different. It is clearly visible only in females heterozygous for both e and $bran^{dp}$. These females are actually sooty-like, with darkened body and wings. That $bran^{dp}$ is responsible for this enhancing of dominance is proved by crossing a soft blistered fly from poi : dp stock, i.e., $bran^r/bran^r$, poi with ebony; no dominance effect is obtained. In the F_2 recombination $bran^{dp}/bran^{dp}$, e/e the ebony color seemed to be intensified; but since we did not succeed in extracting an intensified line this might have been a chance result.

One more remarkable feature is typical for the poi : dp stock. We discussed above the suppressors for eyeless found in the px bl derivatives (see p. 359). At this occasion we mentioned a case in which eyeless seemed to be partially dominant in the combination bw/bw, e/e, ey/+, + meaning a fourth chromosome from poi stock. This dominance was restricted to the males of this combination alone. The same is typical for poi : dp as found in repeated checks at different times. In table 55 one such series is found. The numbers of the reciprocal classes with ey/ey and ey/+ added together are about equal in the four groups (71, 64, 79, 125, the latter containing the more viable plus class); but there are only two bw e males against 69 bw e ey males. It must be supposed, therefore, that almost one-half of the bw e ey males are heterozygous for ey. The absence of the same effect in the three other groups is probably due to the simultaneous presence of the second- and (or) third-chromosome suppressors, discussed above. (It may be added that the same phenomenon was found in a poi allele, called sl : dp, produced by X rays, which in many respects parallels poi : dp. Its remarkable genetics will be presented separately. The Patterson backcross has been entered in table 55.)

In order to test the explanation involving a shift of dominance, produced either by something in the fourth chromosome of poi : dp (Dubinin effect?) or in the X chromosome of the same (the salivaries are normal), a considerable number of bw e ey males from Patt × (Patt × poi : dp) were crossed with unrelated eyeless females, and other, different, combinations were made as controls. The results were very strange. Actually, one-half of the bw e ey males turned out to be heterozygous for eyeless. But now the dominance effect had disappeared, though with a y,

bw, e, ey mother the heterozygotes for ey in F_3 had otherwise all chromosomes from the Patterson stock, just as the father had them. In another generation bred from eyeless and not eyeless, F_3 males showed again the first breeding true, the second segregating ey and not ey in equal numbers. No explanation can be offered at present for the disappearance of the ey dominance effect. But we remember that these stocks exhibit the phenomenon of so-called mutable genes. We hope to continue the analysis, which is not connected directly with the present work.

The pointed dumpy combination has been analyzed so extensively because it parallels Demerec's so-called unstable genes in *Drosophila virilis* and furnishes, I think, a simpler explanation for those facts. This part of the problem has been discussed elsewhere (Goldschmidt, 1943). I repeat here only the main points.

In a number of papers Demerec (see 1941) described genetic phenomena in *Drosophila virilis* which he interprets as the result of unstable, ever-mutating genes. The best analyzed case is that of alleles at the miniature (small wings) locus. The decisive facts are as follows. Among a series of mt alleles, two, called 3 and 5, showed the phenomenon in question. This means that the offspring consisted of mt individuals, mosaics, and normals, the last-named breeding true, the others not. A mosaic is a fly with more or less miniature patches on normal wings, or with one normal and one miniature wing (see below). Unstable mt appears in three well-defined "suballeles." Of these, mt^b is stable; mt^c produces only miniature and mosaic offspring; and mt^a, normal, miniature, and mosaic offspring. Demerec considers these facts to be the consequence, in mt^a, of instability of the mt gene both in somatic and in germinal cells, and, in mt^c, of instability only in somatic cells. From the size of the mosaic spots and the number of wild-type flies, it is concluded that the "mutability" begins rather late in development and that the mutation is always one from miniature to normal, both in somatic and in sex cells. Furthermore, a series of modifiers exists. One increases the number of normals (called germinal mutability), but only in the mt^a line, which always segregates normals. Another series of modifiers (called S genes) increases only the mosaic spots (i.e., is supposed to act only upon somatic mutability). Without these enhancers a small percentage of flies show mosaic spots, and these spots rarely extend to an entire wing. In the presence of the modifiers the percentage of mosaics is increased up to 95 per cent, and one of the S genes frequently produces flies with one normal and one miniature or mosaic wing. There is, further, a sexual difference in all these effects. Finally, the a, b, c forms may change into one another and in a reversible way.

The first question is whether the series of phenotypes from pointed to dumpy, which we may call, in brief, the poi: dp effect, can be assumed to be comparable to those described by Demerec. There is no doubt in regard to the unchanged wings, i.e., miniature in *virilis*, pointed in my case, or for the type with one wing plus, one mt in *virilis*, one pointed, one dumpy in my case. The decisive types are the mosaic types in *virilis* and the intermediates in my case. Demerec assumes that the mosaic spots of miniature cells are genetically miniature, and the normal wing parts are genetically normal by somatic mutation. If one thinks of such mosaics in a general way, comparing them with gynanders or mosaic spots analyzed by markers, one is led to such an interpretation. But in the case in question this is not conclusive. A miniature wing is essentially one in which cell growth after pupation is inhibited (see Dobzhansky, 1929; Goldschmidt, 1935; Waddington, 1940). If this inhibition has a narrow threshold condition so that it will act only partially in the presence of a certain genetic condition, a mosaic-like structure of the wing will appear in the varying and asymmetrical patches of miniature tissue, including also the normal and the + : mt wings. Actually, we know of no case of a real mosaic within a wing, but many cases in which such an asymmetrical threshold effect occurs (see my discussion of the nicking effect, in Goldschmidt, 1940, pp. 222 ff.). In my case the decision is between a pointed and a more or less truncated wing. As truncation is a phenomenon at the wing edge, no mosaic in a plane can become visible. The mosaic produced by the transgressive threshold action appears in the form of a wing edge showing all transitions from pointed to dumpy, more or less asymmetrically. Thus, I believe that also in the miniature case there is no necessity for the assumption that the normal wing cells are genetically different from the miniature cells. A threshold condition acting within narrow limits can produce the apparent mosaic within the genetically miniature cells.

The data in my case indicate clearly the reason for the variable effect. The bran^{dp} allele, interacting with the svr^{poi} locus, is responsible for the threshold condition. Other bran alleles have a truncating effect alone, and, together with svr ^{poi}, produce wing types such as soft blistered, truncated blistered, rudimentary blistered, etc. But bran^{dp} is an allele which alone has no visible effect, but with svr^{poi} hardly succeeds in pushing the pointed wing over the threshold toward a dumpy wing. In other words, the bran allele acts near the level of epistasis for whole wings or parts of them. In our case the explanation is clear: (1) a combination of two interacting loci; (2) the presence of one allele affecting epistasis near the threshold level; (3) the developmental physiology of the wing. As the parallelism with miniature is practically complete (including also modifiers and sexual difference), I conclude that mt^{e} collaborates with another allele which, like bran^{dp}, has no visible action alone, but, if epistatic, pushes wing-cell development toward normal, just as bran^{dp} pushes it toward truncation, and further, that mt^{e} is not an mt allele but ordinary mt in the presence of the other locus, say e, which has an epistatic action near the threshold.

In my case the location of bran^{dp} in the arc region is clear because alleles with visible action exist. In Demerec's case the second locus e is difficult to locate because it also had no action alone, and no alleles with visible effect have been reported. It might even be linked with the miniature locus, as is suggested by some data. But there are no general difficulties to an understanding of mt^{e} without unstable genes.

We turn now to mt^{a}. Here the other group of facts found in my case comes in. It turned out that within the poi : dp stock an allele of bran is present frequently, or occasionally, called bran^{r}, which, together with svr^{poi}, produces a wing with a phenotype like rudimentary and blistered. This combination is, as we saw, less viable and, if produced by mating bran^{dp}/bran^{r}, appears in less than one-fourth of the expected number, sometimes in only a few individuals. The allele bran^{r} alone produces a kind of truncated wing. The segregating bran^{r}/bran^{r}, svr^{poi} flies breed true. Returning to our former comparison of the two cases, the svr^{poi} locus paralleled the mt locus in *virilis;* bran^{dp} paralleled an unknown locus in *virilis* with the discussed effect upon epistasis, otherwise producing a normal wing. If we had now, in addition, another allele of the latter (called e) which, if homozygous, produces complete epistasis of its normal effect over the mt effect, thus paralleling the action of bran^{r}, true-breeding normal flies would result from this combination mt/mt, e′/e′. A line containing e and e′ with a chance for segregation of e′/e′ would be the complete explanation for Demerec's mt^{a}, throwing the "mutation" to normal.

The alleles bran^{s} and poi si.—In the section on mutation (below), mutational changes in a stock 369 of px bl will be related which parallel those reported in the Introduction. Among others, normal flies without px and bs appeared as before. Two such pairs were mated, the males showing indications of being px/+. The offspring consisted of (no. 4482) :

+	50 ♀ 38 ♂
poi	12 ♀ 18 ♂
poi sing	11 ♀ 4 ♂
px	9 ♀ 11 ♂
px poi blist	15 ♀ 11 ♂

Thus both parents were heterozygous for px. The female was heterozygous for poi and the male had been poi without showing it. Moreover, something segregated which made the major part of the females and half of the males with poi singed (singed area on wings) or, in the presence of px, blistered. It turned out that, simultaneously with the "return mutation" of px and bs, a poi and a bran allele had arisen, the latter in a chromosome either with or without px. The pointed and singed individuals bred true and furnished the stock 4902 poi sing, which bred true to pale, pointed flies, the majority of which had singed spots on the wings. Modifiers existed for the penetrance of singed which could be selected back when it became scarcer in the stock. Another stock containing the same constituents and px in addition was bred as 4918 poi sing px; here the singed wing area was frequently

replaced by a blister. Poi was clearly visible with px. The analysis made by crossing the stocks to +, different poi, and different bran alleles, and other tests, showed that a new bran and a new poi allele were present. The bran allele (like $bran^{dp}$, above) alone has no visible effect in homozygous condition. It was called $bran^{s}$. The poi allele alone cannot be distinguished from standard poi by its phenotype; it was called $svr^{poi\ s1}$. The combination of both homozygous (♂♂ hemizygous) gives the phenotype as described. If the compound bran/$bran^{s}$ is combined with poi si, the flies fluctuate from a pointed singed over a more or less soft blistered to an extremely blistered (when newly hatched) and completely folded wing. This and the other combinations show $bran^{s}$ to be a lower allele, but poi si higher than poi. The flies with poi si are also paler. If homozygous bran is combined with poi si, all flies are of the extremely blistered and folded type. In table 74 a number of such combinations are desribed. One remarkable feature of poi si is that it suppresses speck completely in the females but very incompletely in the males, whereas, other alleles have a tendency to the opposite behavior.

The allele poi dish.—From the same stock from which $bran^{s}$ and poi si had originated, another remarkable allele of poi was obtained, again in a strange combination. A pair of low px flies (the stock had previously been extreme px and bl) were mated. Three-fourths of the progeny (4489) were of the parents' own type, and one-fourth were pointed pale blistered and plexus flies exactly like those described as the combination $bran^{s}$ px/$bran^{s}$ px, poi si. The latter bred true (4679) in about half of their offspring, the other half not being blistered. F_3 was bred from both these types, and the offspring in two broods from each type were practically identical, namely, the px poi blist type, but with varying numbers of blisters (4948–51), showing that blistering had a fluctuating expression. In one of these (4948) from not blistered parents the majority of females had either an abnormal abdomen of the type found in higher bb alleles or in the a px deficiency (etched with various amounts of larval chitin present). One other brood contained some of these types. The brood 4938 bred true to type, including the abdomen effect (achi = achitinous). But in later generations the achi effect was somehow selected out and the established stock bred true to the new type without the persistence of larval chitin (stocks 5160 and 4949). The new character of this line is extremely pale color, far beyond that of poi, and a reduction of the dark bands at the posterior edge of the abdominal tergites. Simultaneously, the larger hairs of this fringe are reduced in number and size, and appear irregular, bent, or crooked; the small hairs of the tergites are also involved. In extreme cases all hair is straggling and disheveled, from which the symbol poi dish has been derived. It turned out that the abdominal achi effect had nothing to do with the disheveled hair effect, but was produced by a bb allele, which seems to have arisen simultaneously (see details below). This was proved by combining poi dish with bb. The abdominal effect is influenced by poi dish so far as the imaginal chitin tends to be localized at the posterior edge of the tergites, the same edge which poi dish alone affects. Poi dish contained also the $bran^{s}$ allele which, together with px and poi, produced the narrow blistered wings. $Bran^{s}$ also enhances the poi dish effect, which is most pronounced with homozygous $bran^{s}$. Thus the new svr^{poi} allele $svr^{poi\ dish}$, appeared in the presence of $bran^{s}$ and together with a bb allele.

The same poi dish allele was obtained once more under similar circumstances. An achi stock had been built up from a combination of one bb allele introduced with a

TABLE 74

PHENOTYPES OF bran, poi, AND bran poi COMPOUNDS AND COMBINATIONS

(Descriptive name in italics. If not mentioned, the first-chromosome locus includes both homozygous females and hemizygous males.)

2d chromosome	1st chromosome	Phenotype
bran/bran	+	*broad round* = *bran*
bran′/bran′	+	Normal, broader
$bran^2/bran^2$	+	*broad round* = *bran* (more angular?)
Bran/+	+	Like bran
bran′/bran	+	Like bran
bran′/arc	+	Almost like bran
Bran/bran	+	Like bran and Minute
Df apx/bran	+	exaggerated, ♂ frequently scalloped
Df apx/bran′	+	Like Df apx/+
Df apx/$bran^2$	+	Like Df apx/+
+	svr^{poi}	*pointed* (*poi*) (all svr alleles pale)
+	$svr^{poi\,h}$	More pointed than svr^{poi} (all svr alleles pale)
+	$svr^{poi\,bl}$	pointed
+	$svr^{poi\,s}$	Not very pointed, *soft*
+	$svr^{poi\,sq}$	± pointed
bran/bran	svr^{poi} or $^{poi\,h}$	*soft blistered* and shortened
bran/bran	$svr^{poi\,bl}$	*pointed blistered* = *poi bl*, long wings
bran/bran	$svr^{poi\,s}$	soft blistered, many dumpy rudimentary blistered
bran/bran	$svr^{poi\,sq}$	short dp–rud bl and also soft blist
Bran/bran	$svr^{poi\,bl}$	soft blist and Minute
$bran^2/bran^2$	$svr^{poi\,sq}$	broad incl. to square, truncated; most blistered = *bran blistered*
Df apx/$bran^2$	$svr^{poi\,sq}$	Minute, about one-half dumpy blistered, one-half like bran blist±
$bran^2/bran^2$	svr^{poi}	soft blistered
bran′/bran′	$svr^{poi\,s}$	*slender*
bran/+	$svr^{poi\,s}$	*slender and singed* (part of indiv.)
bran′/+	$svr^{poi\,s}$	*slender and singed* (part of indiv.)
bran′/bran	$svr^{poi\,s}$	*slender and singed* (part of indiv.)
$bran^2/+$	$svr^{poi\,s}$	Some slender with basal blisters = *slender blistered*
$bran^2/bran^2$	$svr^{poi\,s}$	slender blistered–soft blist
Bran/$bran^2$	$svr^{poi\,s}$	*rudim. blist*
$bran^{dp}/bran^{dp}$	+	Normal
$bran^{dp}/+$	+	Normal
$bran^{dp}$/bran	+	Normal
$bran^{dp}/bran^{r}$	+	broad round toward dumpy
$bran^{r}/bran^{r}$	+	broad round toward dumpy
$bran^{r}/+$	+	Normal
$bran^{r}$/bran	+	broad round
$bran^{dp}/bran^{dp}$	svr^{poi}	*pointed dumpy* = poi:dp, transitions poi–poi:dp–dp–dp blist
$bran^{dp}/+$	svr^{poi}	pointed
$bran^{dp}$/bran	svr^{poi}	pointed
$bran^{dp}/bran^{r}$	svr^{poi}	pointed dumpy, etc. (poi:dp)
$bran^{r}/bran^{r}$	svr^{poi}	rudimentary blistered and soft blistered (more former)

TABLE 74—(*Continued*)

2d chromosome	1st chromosome	Phenotype
$bran^{r}/+$	svr^{poi}	pointed
$bran^{r}/bran$	svr^{poi}	rudimentary and soft blistered (more latter)
$bran^{dp}/bran^{2}$	♀ poi/poi^{sq} ♂ poi	♀ like poi:dp but majority poi; ♂ the same, still fewer not poi
$bran/bran^{2}$	♀ poi/po^{sq} ♂ poi	♀ dumpy and dumpy blist; ♂ few the same, most soft blist
$bran^{dp}/bran'$	♀ poi/poi^{s}	*slender*
$bran^{dp}/bran^{2}$	♀ poi^{s}/poi ♂ poi^{s}	Like poi:dp, ♀ poi:dp singed
$bran'/bran^{2}$	♀ poi^{s}/poi^{sq} ♂ poi^{s}	♀ between bran blist and soft blist; ♂ most soft blist
$bran'/bran^{2}$	♀ poi/poi^{sq} ♂ poi	soft blist
$bran^{r}/bran^{2}$	♀ poi/poi^{sq} ♂ poi	♀ dumpy–bran blist; ♂ dumpy blist–soft blist
$bran^{dp}/bran^{dp}$	♂ poi^{sq}	dumpy blist (?)
$bran^{r}/bran^{r}$	♂ poi^{sq}	soft blist (?).
$bran^{2}/bran^{2}$	♀ poi^{s}/poi^{sq}	Between soft blist and bran blist
$bran^{db}/bran^{2}$	♀ poi^{s}/poi^{s}	soft blistered
$bran^{db}/bran^{2}$	♀ poi^{s}/poi^{sq}	dumpy blistered
$bran^{db}/bran^{db}$	poi^{sq}	dumpy blistered (sometimes var. to soft bl.)
$bran^{db}/bran$	♀ poi^{s}/poi	soft blistered
$bran^{db}/bran$	♀ poi^{sq}/poi	dumpy blistered
$bran^{db}/bran$	♀ poi^{sq}/poi^{sq} ♂ poi^{sq}	soft folded (blist)
$bran^{db}/bran^{db}$	poi/+ or +/+	bran
$bran^{db}/bran$	poi^{sq}/+	bran
$bran^{3}/bran^{3}$	+	Normal
$bran/bran^{3}$	+	Normal
$bran^{2}/bran^{3}$	+	Normal
$bran/bran^{3}$	♀ poi/poi ♂ poi	pointed, some singed or blistered
$bran/bran^{3}$	poi si	poi sing–soft blist–very blist folded
$bran^{3}/bran^{3}$	poi si	*pointed singed*
bran/bran	poi si	Very blist folded
$bran^{2}/bran^{3}$	poi si	pointed soft, blister in V
$bran^{1}/bran^{3}$	poi si	± pointed singed
$bran^{1}/bran^{3}$	poi si	poi sing–soft blist–very blist folded
a px/a px	poi si	pale plexus blistered arc
$bran^{3}$ px/$bran^{3}$ px	poi si	pale pointed plexus blistered
+/+	poi si	pale pointed
$bran^{3}/+$	poi si	pale pointed
+/+	poi dish	*very pale, pointed disheveled* ♀ more than ♂
$bran^{3}$ px/$bran^{3}$ px	poi dish	narrow, plexus, blistered, pointed, very pale, very disheveled
bran/bran	poi dish	soft blistered, dwarfish, very pale, etc.
$bran^{3}$ px/$bran^{3}$ px	poi si/poi dish	Like poi dish with $bran^{3}$
$bran^{2}/bran^{3}$ px	♀ poi/poi dish ♂ poi dish	Only few ♀ singed, poi dish ± dominant, ♂ var. to soft blist
$bran/bran^{3}$ px	poi/poi dish	poi dish ± dom; few ♀ blist in V
$bran^{1}/bran^{3}$ px	poi^{sq}/poi dish	poi dish ± dom; no blisters
$bran^{3}/+$	poi/poi dish	poi dish ± dom
$bran^{2}/bran^{2}$	poi dish/poi dish	poi dish type but dumpy with basal blister like bran blist–poi bl–soft blist
$bran^{4}/bran^{4}$	+	Like bran, varying toward ±
$bran^{4}/bran^{3}$	+	Between + and bran
$bran^{4}/bran^{4}$ or ^{3}	poi bl	pointed ± singed–blist
$bran^{3}/bran$	poi dish	poi dumpoid–poi sing–almost soft blist
$bran^{3}/bran'$ or ^{dp}	poi dish	Very few sing
bran/bran	poi dish	soft folded, blist ?

pointed X chromosome and another introduced by a px sp (see section on bb), a stock in which all females had the achi abdomen together with short bristles. This stock was outcrossed to standard pointed, and in the offspring poi dish appeared, i.e., again in the presence of the arc, bobbed, and the svr^{poi} mutant loci. Analysis showed it to be identical with the 5160 poi dish allele. More details will be given in the section on mutation. The new mutant poi dish was checked for allelism to poi and for sp suppression, with positive results. The presence of bran^{3} was revealed by the same checks as are presented in the foregoing section. The irregular presence of a bb allele with no visible effect when alone and only a slight compound effect with standard bb was also found. As these crosses (actually very elaborate because originally the relations of bran^{3} to achi and bb were not known) do not show anything new; they will not be tabulated; and only some of the combinations are entered in the table (74) of phenotypes.

When these experiments were performed, still another bran allele was found, bran^{4}. As not much is known of it, only the known phenotypes have been entered in table 74. Its origin will be discussed below in the section on mutation.

Table 74 tabulates all the phenotypes of the bran or poi alleles and their combination effects studied in the foregoing pages.

Bobbed in the pointed stocks.—We have already mentioned the fact that a bobbed allele was found in the pointed stocks, but no short bristles, the bristles actually tending to be longer than usual. But in the offspring from pair matings, flies were sometimes found with etched abdomen, which is one of the phenotypical expressions of the bb mutants, though usually this character is found only in the higher alleles with shortened bristles. Here it was present with normal bristles. As this etching is the lowest expression of incomplete imaginal chitinization, i.e., persistence of larval chitin, we call the phenotypes beginning with a little etching of the tergites and leading through all transitions to abdomina with nothing but larval chitin the *achi* type (achitinous). To give an example for svr^{poi}: Among the offspring of 20 pair matings, 8 contained these etched (low achi) flies (only females), namely, once 1 among 43, once 15 among 71, once 5 among 72, and 5 times, the majority of the females. By crossing to the bb alleles, it was found that an allele of bb was present which in homozygous condition had no bristle effect, though some achi effect, as stated; but in compounds with other bb alleles the bristle effect became visible.

When it was found that px bl, as well as svr$^{poi\ h}$ of completely unrelated origin, sometimes also contained a bb allele, and furthermore, that remarkable relations obtained between the svr alleles and bb (see the foregoing section on poi dish), we made a closer study of the bb locus in the stocks of svr alleles. This study was partly facilitated, partly complicated, when it turned out that the standard a px sp stock contained bb alleles which in compound with those from poi produced a high and even extreme achi and bb phenotype, though otherwise they had hardly any visible effect. As tester stocks two bb stocks were used, kindly furnished by Professor Curt Stern, one marked with yellow garnet (y g bb), with a very small phenotypic effect, the other a bb^{1} stock carried as ClB/w^{e}bb^{1}, with rather variable effect but powerful in compounds (probably a deficiency). To avoid lengthy descriptions, all phenotypes of homozygous or compound females relevant for the present analysis are presented in table 75. A comparison of the different phenotypes explains the results of the genetical analysis. It ought to be added that the phenotype is rather modifiable both

TABLE 75

PHENOTYPES OF bb ALLELES AND COMPOUNDS

No.	bb allele		Origin		Phenotype ♀	
	X^1	X^2	X^1	X^2	Bristles	Abdomen
1	bb	bb	y g bb	y g bb	+–bb 1	+–achi 1
2	+	bb^1	ClB	bb^1	+ and some bb 3	+–achi 1
3	bb^1	bb	ClB/bb^1	y g bb	bb 2–3	achi 3–4
4	bb	bb^{poi}	y g bb	poi dish 5145	bb 1–2	+–achi 2
5	bb	$bb^{poi\ hi}$	y g bb	poi dish 5145	bb 4–5	achi 5
6	bb^1	bb^{poi}	ClB/bb^1	poi dish 5145	bb 2–3	achi 2
7	bb^1	$bb^{poi\ hi}$	ClB/bb^1	poi dish 5145	bb 5	achi 4–5
8	bb	$bb^{a\ px\ sp}$	y g bb	5144 a px sp achi	bb 1–2	+–achi 2
9	bb^1	$bb^{a\ px\ sp}$	ClB/bb^1	5144 a px sp achi	bb 4	achi 4
10	bb	$bb^{a\ px\ sp}$	y g bb	a px sp	bb 2	achi 1–3
11	bb^1	$bb^{a\ px\ sp}$	ClB/bb^1	a px sp	bb 2–4	achi 3–4
12	$bb^{poi\ hi}$	$bb^{a\ px\ sp}$	poi dish 5145	a px sp	bb 3–4	achi 3–4
13	$bb^{poi\ hi}$	bb	From achi ♂ 6317	y g bb	bb 2–4	achi 3–4
14	$bb^{poi\ hi}$	$bb^{poi\ sq}$	5144 a px sp achi	poi sq 5121	(2d chr. a/$bran^2$) bb 5	achi 5
15	bb^{poi}	$bb^{poi\ sq}$	5144 a px sp achi	poi sq 5121	(2d chr. a/$bran^2$) bb 2–3	achi 2
16	bb	$bb^{poi\ sq}$	y g bb	poi sq 5121	(2d chr. a/$bran^2$) bb 1–2	achi 1–2
17	bb^1	$bb^{poi\ sq}$	ClB/bb^1	poi sq 5121	(2d chr. a/$bran^2$) bb 5	achi 5
18	bb^{poi}	bb^{poi}	From crossover y g bb and poi		like bb	like bb
19	bb^1	+	ClB/bb^1	a px sp	(2d chr. a/a) +	+
20	bb^{poi}	$bb^{poi\ hi}$	poi dish 5145	poi dish 5145	(2d chr. $bran^2$/$bran^3$) bb 4–5	achi 4–5
21	bb^{poi}	$bb^{a\ px\ sp}$	poi dish 5145	poi dish 5145	(2d. chr. $bran^2$/$bran^2$) bb 1	achi 1–2
22	bb^{poi}	$bb^{a\ px\ sp}$	poi dish 5145	poi dish 5145	(2d chr. $bran^1$/$bran^1$) bb 2	achi 1–2
23	$bb^{a\ px\ sp}$	$bb^{a\ px\ sp}$	5144 a px sp achi	5144 a px sp achi	(2d. chr. $bran^{dp}$) + and bb 1	+–achi 1
24	bb^1	$bb^{a\ px\ sp}$	ClB/bb^1	5144 a px sp achi	(2d. chr. a/a) bb 2–4	achi 3–4
25	bb	bb	y g bb	y g bb	(2d. chr. all bran alleles) +	+
26	bb^1	+	ClB/bb^1	Diff. stocks	(2d. chr. all bran alleles) like bb^1/+ +/+	like bb^1/+ +/+
27	bb^{poi}	$bb^{poi\ hi}$	Diff. stocks	Diff. stocks	bb 4–5	achi 3–5
28	$bb^{a\ px\ sp}$	$bb^{a\ px\ sp\ hi}$	5144 achi a px sp	5144 achi a px sp	bb 4–5	achi 3–5
29	bb^{poi}	bb^{poi}	Diff. stocks	Diff. stocks	+	+–achi 1
30	$bb^{a\ px\ sp}$	$bb^{a\ px\ sp}$	5144 achi a px sp	5144 achi a px sp	+–bb 1	+–achi 1
31	$bb^{poi\ hi}$	$bb^{poi\ hi}$	Diff. stocks	Diff. stocks	Lethal	Lethal
32	$bb^{a\ px\ sp\ hi}$	$bb^{a\ px\ sp\ hi}$	5144 achi a px sp	5144 achi a px sp	Lethal	Lethal

Legend:

bb 1–5: little, ¼, ½, ¾, complete, shortening of bristles.

achi 1–5: little etching, more etching, large patches of larval chitin, more larval than imaginal chitin, almost no imaginal chitin.

5144 a px sp achi = stock with high incidence of bb achi derived from backcrosses (a px sp × poi) × a px sp containing compounds of the respective bb alleles.

5145 poi dish = stock of same derivation containing the later-arisen mutant poi dish and freed from a px sp by outcrossing to poi; contains both bb alleles from poi.

poi sq 5121 = stock broad blistered = $bran^2$/$bran^2$, $svr^{poi\ sq}$.

6317 derived from 5144 with ♀ and ♂ bb achi.

by environment and by genetic modifiers, and hence that many repetitions of crosses and selections in extracted stock were required for determining the genetical basis of the observed results.[6]

In the a px sp stock the bristles are normal, but individuals with more or less etched abdominal tergites, i.e., beginning and low achi, are frequent. Occasionally, a fly appears with higher-grade achi, and once a female extreme achi and bobbed was found. The explanation will be given below. As table 75 (nos. 8–13) shows, most flies from a px sp stock contain a bb allele, some are heterozygous for it, and some are free from it. This allele in homozygous condition has no bristle effect, which is also true for other alleles; but the bobbed character appears in all compounds with other alleles, also in those which themselves have no bristle effect. This strange behavior was found for all lower bb alleles used in this work, and only the higher ones showed a homozygous effect. The achi effect of the compounds generally parallels the bristle effect, though one might say that as a rule the shortening of the bristles is one step ahead of the increase in the achi character. But it turned out that the presence of homozygous arc acts as an enhancer of the achi effect. This is remarkable because a deficiency in the arc region—Df(2) a px—also has an achi effect, together with the bristle effect of the Minutes. We shall return to this point later. It further turned out that sometimes a px sp contains a higher bb allele which is either completely or almost lethal in homozygous condition, and which in compounds reduces viability considerably. The compound of the two alleles looks high to extreme bb and achi, especially in the presence of arc. There is reason to believe that this allele originates frequently by mutation in the stock. Males with the high allele are viable, and thus apparently true-breeding lines may be obtained from compound females and genetically high males, the homozygous high females being lethal. We call these alleles $bb^{a\ px\ sp}$ and $bb^{a\ px\ sp\ h}$, the former being a little higher than the standard bb used here (y g bb). Both give the expected exaggerated effect in compound with bb^{1}. Also, males with the high allele $bb^{a\ px\ sp\ h}$ have a tendency to show beginning achi in the genital segment (up to 10 per cent of the males).

The bb allele present in poi turned out to be a little lower than $bb^{a\ px\ sp}$. Again, it has no bristle effect in homozygous condition, but in compound with $bb^{a\ px\ sp}$, i.e., $bb^{a\ px\ sp}/bb^{poi}$, a low bristle and achi effect appears, and a high one in compound with $bb^{a\ px\ sp\ h}$. Whenever, from a cross involving these alleles, homozygous $bb^{a\ px\ sp}$ or bb^{poi} segregates together with the compound, we have one-half normal, one-half bb achi flies, a fact which caused much confusion before the compound action had become clear.

Both in crosses between poi and a px sp and in selections of poi exhibiting the achi character, a high allele of bb was sometimes also found in the poi chromosome. Thus, it was found when poi dish originated (see above), and it was also present occasionally with other poi alleles, especially poi sq. Its action upon the phenotype is about midway between bb and $bb^{a\ px\ sp\ h}$. Thus the increasing order of the alleles derived from the bb and achi effect is bb (y g bb)–bb^{poi}–$bb^{a\ px\ sp}$–$bb^{poi\ high}$–$bb^{a\ px\ sp\ h}$.

As we have said, arc enhances the achi effect. Therefore, all bran alleles were combine with bb and bb^{1} to compare their effect. It turned out that no enhancing was observable except with $bran^{2}$ (which is a one-band deficiency) in compound with arc. But, strangely enough, homozygous $bran^{2}$ did not enhance the effect. We

[6] Some of the facts presented here have been made the subject of a special contribution to Amer. Nat., December, 1944.

therefore also tested the Df(2)a px (which alone is Minute with a little achi) with all available bb alleles, but we could not discover any enhancing effect in the presence of homozygous or heterozygous bobbed alleles.

Finally, the phenotypic combination of $bb^{poi\ high}$ in the presence of poi dish must be mentioned. Whereas the high-grade achi abdomina show all kinds of irregular patches of imaginal chitin on the basis of white sections of larval chitin, in the presence of poi dish the imaginal chitin is always preserved dorsally at the posterior edge of the tergites. We have described above the effect of poi dish upon the chitin and bristles of these same edges, an action which thus in some way controls also the localization of the achi effect.

At the time of the discovery of bb it was found (see Morgan and Bridges, 1916) that hereditary bobbed males occasionally appeared, which was interpreted as a mutation of the $+^{bb}$ allele in the Y chromosome to bb. The same phenomenon was observed repeatedly both in $bb^{a\ px\ sp}$ and in bb^{poi}, and also in the higher alleles. The responsibility of the Y chromosome was easily ascertained in crossing to y and further generations in which the Y chromosome alternates from males to females with the consequent effect upon males. But it seems that the explanation by mutation in the X chromosome does not suffice, as cases were found where the bb achi males contained an X chromosome without bb. Other peculiarities, such as a huge enhancing effect upon bb males by a Dichaete third chromosome, are only mentioned. Still more remarkable is the fact that males with bb^1 in the X chromosome and the mutated Y which makes bb visible are normal. But such facts do not belong here.

Finally, it happens very frequently that in crosses which ought to yield only normal or low bb flies a few individuals with high bb achi appear. When tested, they always turn out to be compounds of the low bb introduced into the cross and a high bb allele which must have arisen by mutation, which thus seems to be a rather frequent occurrence in bb chromosomes whether derived from our poi stocks or not.

I point out again that bb was found in px bl and in poi, poi h, poi sq, all of more or less different origin, and that a relation was repeatedly found between the appearance or presence of bb and the mutation at the bran and poi loci. The data are presented in the appropriate sections.

d. NOTES ON THE PHENOTYPE OF WING SHAPE

In the foregoing pages we have described a number of wing types which are obtained when mutant loci for pointed and for broad and shortened wings collaborate. Different conditions obtained according to the alleles and loci involved—conditions which might be described in general terms as different degrees of epistasis including threshold phenomena. Similar phenotypes are produced also by the collaboration of different loci with visible effects comparable to those of poi and bran. In all cases the mutant predominantly affects the posterior wing margin. One group of mutants, namely, the pointed alleles at the silver locus (first chromosome), and the lanceolate alleles (second chromosome), produce more or less pointed wing tips in the lower grades and a retraction around the end of the fifth longitudinal veins, which results in narrow slender wings in the higher grades. I have shown in an earlier work (Goldschmidt, 1937) that such wings are normal at the time of pupation but soon afterward produce the pointed tip by a kind of contraction, which I considered to be associated with the histolysis of subepidermal tissue, whereas Waddington

(1942) thinks that only contraction is involved. Furthermore, the pointed phenotype can actually be obtained as a so-called phenocopy by treating normal late larval and early pupal stages with heat shocks (Goldschmidt, 1935). The phenocopies obtained in a complete series of grades are exact copies of the phenotype of the first-mentioned mutants. The other group of mutants studied here, namely, the bran alleles in the arc region of the second chromosome and rudimentary in the first chromosome, produce more or less truncated wings (like the mutant dumpy and other similar ones), wings in which the tip shortens, and the posterior edge curves in giving the wing a broadened appearance. Moreover, the wing appears to grow only to more or less of its full length, thus producing all transitions from a long, slightly truncated, to a very short rudimentary wing of essentially the same form. It has been shown by Auerbach and by me (Auerbach, 1936; Goldschmidt, 1935) that truncated wings are normal at the time of pupation, but afterward retract in their sheath to form a truncated and shortened wing, while a cytolysis of subepithelial tissue takes place. Waddington (1940), however, assumes that the wing appears normal at the time of pupation only because it is overinflated, and that it later retracts to a predetermined dumpy form. This is not the place to discuss these different interpretations of identical facts, but I have many reasons to doubt Waddington's interpretation. Also, this type of truncated wing may be produced as phenocopy by heat shocks (Goldschmidt, 1929, 1935; confirmed since by many authors). In this case all transitions may be obtained from a pointed-like wing to one intermediate between pointed and dumpy to typical truncation, thus showing that the sharpening and truncating features are based more or less on closely related embryological processes (with which my embryological observations, loc. cit., agree).

This comes out clearly when wing-broadening (bran and alleles) and wing-sharpening mutants (pointed and alleles, lanceolate) are present simultaneously; in this case the sharpening process in development combining with the broadening one may lead to a regular truncation. In detail, however, a great many different possibilities are realized, depending upon the amount of epistasis of the two loci involved, i.e., their relative influence at the critical time in development, which probably means definite threshold conditions (see discussion of the poi : dp phenotype above). At the one end of the line of possibilities actually realized we find the combination of svr^{poi} with rudimentary. As reported above, both pointed and a rudimentary allele $r^{px\ bl}$ arose simultaneously from px bl stock. The $r^{px\ bl}$ was at once mated to y and kept as a stock. One such stock (see below) always showed short rudimentary wings, whereas others had long, dumpy-like wings, and one actually reverted to a normal phenotype though genetically it was still $r^{px\ bl}$. The short rudimentary turned out to contain also pointed, which bred with y, could not be lost by crossing over. In this case either rudimentary, i.e., extreme truncation, was completely epistatic over pointed, or, more probably, truncated was epistatic, but pointed acted simultaneously in the combination by still further shortening the rudimentary wing besides producing blisters. We remember that exactly the same phenotype, called rud blist, was also the result of the combination of certain bran alleles and compounds with svr^{poi} and alleles (see table 74). In these combinations of two different loci, one for sharpening, one for truncating, the wings were symmetrical at the high level of shortening described as rudimentary. At the same end of the epistatic series are such combinations as bran blistered (see table 74) with symmetrical broad

wings (sometimes just beginning truncation), which may or may not show the influence of the poi allele by a symmetrical or one-sided blister. At the other end of the epistatic series, i.e., epistasis of the poi effect (sharpening) over the truncation effect, are such combinations as poi blist where the allele $svr^{poi\ b1}$ with bran produces pointed wings, partly with blisters but without any truncation, and others found in table 74. Between these two extremes all grades of intermediate and variable epistasis relations can be found, and among them asymmetry is a typical feature. Thus bran/bran, svr^{poi} is the type soft blistered. Most wings are pointed but at the same time shortened (and blistered). All transitions appear from pointed to broader wing tips. A small, varying percentage has either one wing short pointed blistered, the other truncated or even rudimentary, or both wings truncated or rudimentary. In the latter case there is usually no clear epistasis, but a kind of compromise between the two wing types. The embryological processes must be such that near a certain threshold the truncating influence wins out, and this threshold is obviously so narrow that it may be passed by one wing and not the other, owing to the small right–left differences in differentiation, well known to the embryologist. For an interpretation of all these phenomena in terms of the physiology of development see the discussion in my book Physiological Genetics (1939), where a dynamic explanation is derived from other cases of the same general type.

A last group shows the developmental reactions and processes of sharpening and truncation, both limited to so short a time of alternative determination (which means the same as a narrow threshold for epistasis) that a variation is found in epistasis from individual to individual, from pointed through all transitions to truncated wings, with, in the transitory group, asymmetrical behavior of the two wings. This group is represented by the combination of $bran^{dp}$ with pointed (the poi : dp case), but it is also represented by a combination of bran with a completely different locus for pointed wings, lanceolate (ll) in the same second chromosome (see p. 309). Finally, also, the combination of rudimentary with pointed, which is usually of the phenotype short rudimentary blistered, may show, in certain genetic conditions to be reported below, all transitions, symmetrical and not, from a pointed to a rudimentary wing. Thus, this entire group of phenotypes presents a good illustration of the phenomenon of epistasis based upon an embryological threshold at the time of wing differentiation. It shows the different ability of the individual alleles (or, more correctly, their effects) to pass the threshold, and of others to control the more or less narrow time limit in which determinative processes are decided in development, a situation which may produce intermediates and mosaics. We shall not go into further detail here. A comparison of the facts with others analyzed in the book just mentioned shows that a beautiful case could be made out for our interpretation of all such phenomena in terms of interlaced reaction velocities.

e. THE SALIVARY CHROMOSOMES OF THE poi AND bran ALLELES, IN THE svr AND arc REGION

On the basis of the deficiency tests the silver locus is expected to be located to the left of 1C in the first chromosome.[8] In all alleles, including those produced by X rays,

[8] Demerec, in a list of loci located in the salivaries (Carnegie Inst. Yearbook 41), mentions svr as located in 1B5, 6, which is rather far to the left of the Bld break.

the region left of Bld is perfectly normal. But in some alleles the region farther to the right, between the Bld break and the bulb, shows typical disturbances. The only one of these which can be described with certainty is found in the allele $svr^{poi\ s}$. Here a 2- (4-) band inversion of 1E1–4 is always found. These bands are described in Bridges' standard map (1938) as two double bands, the one to the left being thinner, that to the right being rather thick. I think that there exist actually only two bands, the double nature of which is not always visible, being based upon a partial separation of the two groups of perultimate chromomeres of which the bands are constituted (see Kodani, 1942; Goldschmidt and Kodani, 1943). In the heterozygote this inversion looks as pictured in plate 30, figures 5 and 6. One cannot always be sure that the interpretation as a minute inversion is correct. But in the homozygote the order of the thin and thick bands 1–2, 3–4 is clearly reversed, as shown in plate 30, figure 7. Therefore we feel confident that the interpretation is correct.

In some of the other alleles, namely, svr^{poi}, $svr^{poi\ sq}$, $svr^{poi\ dish}$, an abnormality of the same bands is found in practically all X chromosomes (this is never true of the controls), a structure which offers great difficulties of interpretation. The order of the bands 1–2, 3–4 is normal. But the thick band 3–4 is distorted in a way that is difficult to describe. When focusing high and low the band seems normal, but in between a kind of cross or X figure appears, an apparent crossing of 1, 2 with 3, 4. This seems to be the result of two features: first, the arrangement of the chromatin on the surface of the disk-like band (like a ring), and secondly, a dislocation of the two halves of this ring belonging to the two homologous chromosomes by a twist in opposite directions. This means that, viewed from above, the upper rim of the disk in one chromosome is shifted to the right and that of the other chromosome to the left, so that a kind of figure 8 becomes visible. This is pictured in plate 29, figures 4–7, where the same chromosome is drawn at different foci. Our interpretation of these typical aspects, which can hardly be drawn as they appear in focusing, is that the distortion within the disk represents a one-band inversion. This requires the assumption that the left and right surfaces of a single disk are serially different. The new discoveries on the structure of the individual disk (see Kodani, and Goldschmidt and Kodani) make such an interpretation possible, since they revealed the presence of a coil of genonema with an attached series of perultimate chromomeres in a disk (each one double). An inversion of one disk would change the direction of the coil, creating a tension in the state of synapsis. (Consult fig. 6, in Kodani's paper.) Homozygous chromosomes were always normal.

In $svr^{poi\ h}$ a different structure is found, again for the same bands. We did not succeed in finding a satisfactory interpretation. The only certain fact is that these bands are not normal. A few of the varying aspects are figured in plate 30, figures 1–4. Sometimes the structure appears to be in the twisted condition just described. The bands seem to be imbedded in a darker-staining substance.[7]

It is remarkable that in some of the poi alleles a clear inversion or less clear abnormalities are found about 6 bands beyond the supposed location of silver. On the basis of our knowledge of the adjacent yellow and scute regions (see discussion in Goldschmidt, 1944) we may assume that the entire region between the scute

[7] A special discussion of these features is given in R. Goldschmidt and A. Hannah, Proc. Nat. Acad. Washington, 1944.

segment and the bulb is involved in producing the poi phenotype (svr itself has completely normal bands) in the sense discussed in the paper mentioned.

The bran alleles involve the arc region, which is known to be located in the second chromosome between 58B and 58E (see fig. 1 in Bridges, 1937). Actually, the allele bran^2 contained in the combination with poi square described as broad blistered is a clear one-band deficiency for what is called by Bridges 58D6, 7, but which appeared in our slides as only a single band. Figures 1–3, plate 29, represent this deficiency, which was always found in good slides. None of the other bran alleles showed any abnormalities, but unfortunately all the dominant Bran could not be checked.

f. THE CHROMOSOME SECTIONS CONTAINING THE poi AND bran ALLELES AND THE ALLELISM WITH svr AND a (arc)

The silver region.—The section of the X chromosome in which the silver alleles are located contains a number of loci the interrelations of which are not completely clear. In addition to silver there is a group of so-called suppressors, namely, su-s, a suppressor for sable; su^2–s a suppressor for both sable and vermilion; su^3–s, a suppressor for speck also. All three are described as allelic to one another. Another one, su$^{s2\text{-}v\ pr}$, suppresses vermilion and purple, but has not been tested for allelism with the others. There is, further, in this region the break of the Blond translocation. As the silver alleles are pale, all these loci have in common an effect upon pigmentation which is suppressed or diluted either in the cuticle of the entire surface of the fly, excluding hair (silver and alleles), or only in hair and bristles (Blond), or only when another recessive mutant is present which produces a specific pigmentation, namely, sable, vermilion, speck. Sometimes, too, a trident is present (svr); this may be the result of transparency of the cuticle overlying the pigmented epidermal pattern (which itself is probably based upon the arrangement of muscle insertions). Finally, the silver group has the additional action of producing pointed and sometimes soft-textured wings, in different degrees, if at all. Nothing is known of crossing over between all these loci, and it would be difficult to study it except for the specific suppressors. Actually, the phenotypical effects completely overlap (except Blond), since silver and alleles are always pale but not always pointed, silver has or has not the trident which is absent in its alleles, svr does not act as a suppressor, and the suppressors are neither pale nor pointed; but all silver alleles of the poi series are suppressors for speck, incomplete suppressors for sable, not for vermilion. (One, poi si, suppresses sp only in females.) This situation reminds one very much of the condition in the yellow and scute sector near by, e.g., different shades of yellow, yellow or dark bristles, etc., with different alleles and rearrangements. For the yellow and scute cases it is known (see discussion in Goldschmidt, 1944) that sections of about 6–8 bands exist within which mutants without visible chromosome disturbance and those based upon position (rearrangement) effects form a series of alleles. Thus, one should expect a similar situation in the svr region which immediately follows the yellow and scute sections to their right.

The break of the Bld translocation is located in the salivary chromosomes between bands 1C3 and 4. According to Bridges, silver as well as the suppressors are located to the left of the break. For the study of this region there are available, also, L. V. Morgan's deficiency of the tip of chromosome 1, including silver; Dobzhansky's

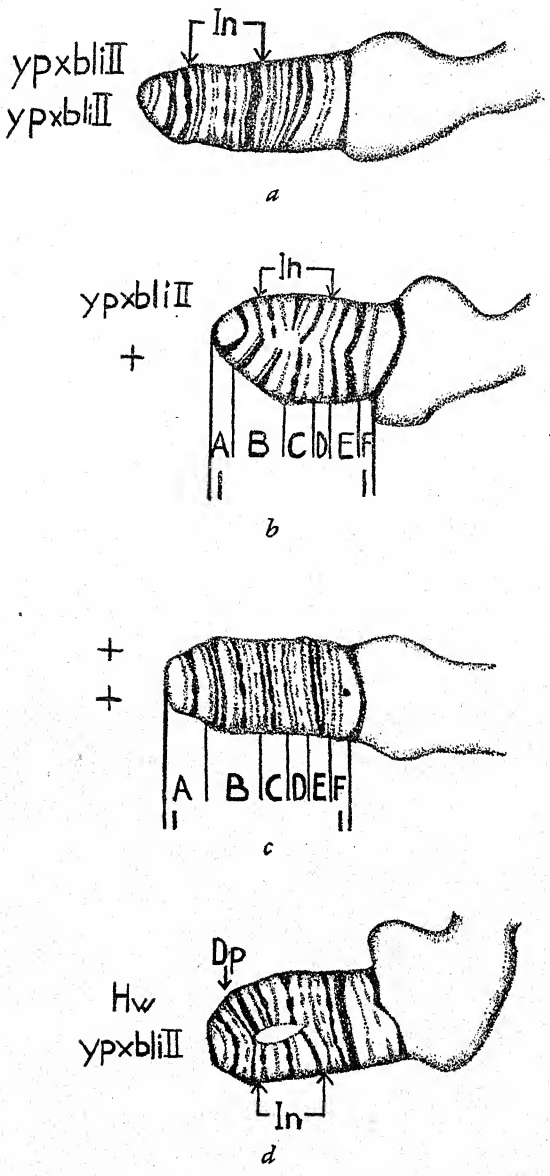


Fig. 3. I(1)$y^{px\,bl}$ = Inversion yellow–px bl in first chromosome 1. *a*. Homozygous inversion. *b*. Heterozygous inversion. *c*. Normal chromosome for comparison. *d*. Inversion opposite Hw duplication. M. Kodani del.

duplication of this region (101), which includes svr and the suppressors; and a new small inversion with yellow phenotype, with the left break in the yellow region, the right break identical with the Blond break (see p. 388, text fig. 3). The pointed alleles which show changes in the salivary chromosomes have the breaks to the right of the Bld break (see above, pp. 395 ff.).

We studied different combinations and compounds to find out the relations between these different mutants. Table 76 contains some of the information. (Only the su^2–s was tested among the suppressors.) The table shows that the phenotypic allelism is more or less clear. It is clear for the silver alleles, but no visible allelism with the su–s exists (the phenotype of this being normal), though the suppressor action for sable is common to both and to the compound, i.e., it is allelic. The haplo effects of the deficiency y–svr are clear, but exaggeration is absent, though occasionally the compounds with the deficiency seemed a little paler. The pointed wing character was never exaggerated. The duplication 101 covers the poi alleles as it covers svr. Only once (for poi s) was it observed that the covering is not complete and that the poi s/Df–Dp flies were paler than normal.

As the break of the Bld translocation is very near to svr and the Bld phenotype is also one of pigment reduction, we tried to see a compound effect between Bld and the svr alleles, but did not succeed. Bld is already paler and tends to a trident rather irregularly. The compounds are not different and there is certainly no pointed effect. The same applies to Inversion $y^{px\ bl}$ with one break identical with that of Bld. But a quite unexpected result was obtained when these rearrangements were combined with bran (remembering that bran together with poi alleles produces blistering.) In the combination bran/T(Bld)1–2, poi/T(Bld)2→1 a soft blistered and Blond male, heterozygous for bran (tested), was obtained once. As bran could not be entered into the Bld second chromosome because it is located too near the Bld(2) break, only the heterozygous second chromosome could be tested. If it were obtained as bran/bran with Bld the effect might appear more clearly. The deficiency (1)Bld with bran in the second chromosome and poi opposite Bld was also not obtained.

But the $yellow^{px\ bl}$ inversion gave a clear result. F_2 from a cross $y^{px\ bl}$ bran segregates ⅛ bran/bran, $y^{px\ bl}$, and these were soft blistered in addition to yellow. *In this case the second break of the inversion showed a position effect typical for the region of the right break together with the yellow position effect of the left break.* Another combination with a similar effect, namely, y–Inv with a dominant Bran, will be described below. The importance of these facts has been stressed in another paper (Goldschmidt, 1944).

The combinations of svr and the suppressor of sable were also tested. Though svr is different from the svr^{poi} alleles with respect to the sp suppression, we were surprised to find a very small combination effect with bran: bran/bran, svr flies are bran and pale, but in a large brood two females had a little blister near the wing tip. Also, the bran/bran, su-s combination was simply bran but had a tendency to soft spread wings, thus showing a poi character not visible in su-s alone.

All these facts show a rather remarkable situation. As a whole, the silver alleles, the sable suppressor (the others were not tested but may safely be assumed to behave similarly), the Blond-translocation break, and the identical right break of the yellow Inversion, act as a series of alleles. As the deficiency and duplication tests show, all the loci are located to the left of these breaks and to the right of the scute

TABLE 76

PHENOTYPES IN THE silver REGION

Mutant or compound or combination	Body color	Trident	Wing shape	Suppressor action	Remarks
svr stock	Pale	....	Varying, poi	.....	pointed and soft wings always clear after extracting from crosses
w^a svr stock	± pale	Present	Not poi	.....	pointed and soft wings always clear after extracting from crosses
All svr^{poi} alleles	Pale	Very rare	poi	Supp. sp and s, not v....	$svr^{poi\,sq}$ ♂ show sometimes trident
su^2–s	+ (= not pale)	....	Not poi	Suppr. s and v.....	
svr/svr^{poi}	Pale	....	± poi	.....	More poi with svr stock, less with w^a svr
$svr/svr^{poi\,s}$	Pale	....	± poi	.....	
svr/su–s	+	....	+	.....	
svr^{poi}/su–s	+	....	+	.....	Also other svr alleles
svr/Df y–svr	Very pale	....	Not very poi	.....	All other svr alleles haploid effect, no exaggeration; all covered by Dp. 101. Only $svr^{poi\,dish}$/Df is lethal
svr^{poi}/Df y–svr	Very pale	....	Not very poi	.....	
$svr^{poi\,s}$/Df y–svr	Very pale	....	Very poi	.....	
svr^{poi}/Dp 101	+	....	+	.....	
Bld/+	Paler than + (Canton)	Frequent	+	.....	
Bld/svr^{poi} and svr	Like Bld	....	.....	.....	
I $y^{px\,bl}$/Df y–svr	Lighter than homoz. Inv.	....	+	I $y^{px\,bl}$ no suppr. action.	
I $y^{px\,bl}$/svr	+	....	+	.....	
bran/bran, poi/poi	Pale	....	See poi alleles	.....	Types soft blistered, etc.
bran/T Bld, T Bld/poi	.....	....	.....	.....	Once a soft blistered and Blond ♂ not def. for chr. 2
bran/bran; I $y^{px\,bl}$/I $y^{px\,bl}$	.....	....	.....	.....	Between soft blist and bran blist (and yellow
bran/bran, svr	Pale	....	bran	.....	Rarely blistered
bran/bran, su–s	+	....	bran	.....	Many soft spread wings

bands. But the minute rearrangements present in some of the alleles (see pp. 395 ff.) are located some bands to the right of these breaks. However, the phenotypical relations of all these alleles and compounds are, I might say, fractioned. Su-s has no allelic effect with svr and its alleles in regard to the character pointed wings and pale color; it is, however, allelic to the svr^{poi} alleles in regard to s suppression. On the other hand, the svr^{poi} alleles are sp suppressors (as are also some of the other unanalyzed suppressors), but they are not allelic to su-s in regard to v suppression present in the latter. The mutant svr is allelic to the poi alleles in regard to pale color and pointed wings, but not in regard to the suppressor action. The break of Blond has a related effect to paleness in svr, acting only on hair. The combination effect with bran (blistering) is extreme in some poi alleles, smaller in others, almost absent in svr, incipient in Bld (no bran/bran tested), and considerable in yellow Inversion. This picture parallels to a certain degree that described for the yellow or black or intermediate hair color and the different yellow body colors in y alleles, and might also be compared to some of the features described for the scute and achete phenotypes. We might express the facts in the following diagram.

Visible effects	Mutants					
	su-s	su-v	svr^{poi} alleles	svr	Bld	y-Inv
Suppression s	———		———			
Suppression sp		———	———			
Suppression v	———					
Pale and poi			———	———		
Blond hair					———	
Combination effect with bran	—	?	———	—	——	———

I consider these facts (as well as the corresponding ones for y, ac, sc) an indication that the concept of the corpuscular gene and its chemical changes in mutation does not cover the actual facts; that, moreover, a chromosome segment of a number of bands is the serial unit in some respects, and that all disturbances within that segment produce a series of multiple alleles. A part of this conception has recently been discussed in Goldschmidt, 1944; a more detailed analysis may yet be given.

The arc region.—The arc region seems to show features similar to those in the silver section. Though we assumed that the bran alleles are alleles of arc, we did not symbolize them as a^{bran}, etc., because the facts do not seem so simple as this. The localization of bran put it at or near the arc locus. No crossover between the two was ever observed, and thus no combination of them was obtained. Bran and plexus, the latter nearest to arc, occurred simultaneously (by mutation) and were closely linked, though rare crossovers occurred just as between a and px. But the compound and deficiency tests did not give a simple result. Table 77 records a number of these tests for bran and some of its alleles. The compounds with arc and with the arc deficiency both indicate allelism. The bran alleles with no considerable phenotypic effect, such as $bran^{1}$, $bran^{dp}$, have little or no effect in the compounds. A remarkable case is $bran^{2}$, which is a one-band deficiency lying inside the rather long a px–Df, as described by Bridges. One should expect the compound to be either lethal or at least of the bran type if not exaggerated. Actually, the compound hardly differs

from the a px deficiency over normal. (If, however, in a backcross the bb allele in the first chromosome of bran blist = bran^2/bran^2, poi^{sq} is added to the compound, an extreme achi bb fly is produced in which the deficiency and bb effect upon the abdomen seem additive.) This is remarkable, as the compounds of bran^2 with bran (see list of phenotypes, table 74) have broad wings, and even the compound with arc is sometimes flapper-like. Certainly, these phenotypes do not fall into line as simply as in other multiple allelic series. Another group of remarkable facts is the following. We saw that many bran alleles give a combination effect with svr alleles,

TABLE 77

PHENOTYPES IN THE arc REGION

Combine	Phenotype of wings
bran/a	Broader than wild type, sometimes variation toward almost bran
bran^{dp}/a	Broader or normal
bran^1/a	Broader or normal
bran^2/a	Almost bran, once broad flapper-like
bran^r/a	+
Df(2)a px/+	Wings broader, some turned up, Minute characters
Df(2)a px/a px	Wings like flappers, turned up (plexation only a little exaggerated), ♀ etched, few blist., all M
Df(2)a px/bran	Variation from broader, part arched to real bran and flapper-like, most males scalloped at posterior edge; all M
Df(2)a px/bran^{dp}	Very broad, part arched; all M
Df(2)a px/bran^1	Almost normal wings; all M
Df(2)a px/bran^2	More like Df/+ than like Df/bran, very few nicked males
Df(2)a px/bran^3	arc-like; all M
Df(2)a px/bran^r	Almost normal wings, part of males scalloped

such as soft blistered, pointed blistered, etc. Homozygous arc with pointed has no such effect, and neither has the Df(2)a px/+ with pointed. But occasionally among Df(2)a px/+ flies without pointed, individuals are found with one dumpoid wing, thus showing a tendency toward a phenotype frequent in bran alleles and combinations with poi. In view of the length of this deficiency this fact may as well be based upon identity as upon a close linkage of the bran and arc loci. Thus, though I believe both to be arc alleles, I cannot prove it beyond doubt and therefore also hesitate to state that the one-band deficiency of bran^2 contains the arc locus. I suspect that we are dealing with a case comparable to that discussed for the svr locus, i.e., the presence of a number of bands with consequent arc or broadening effect caused by visible rearrangements or invisible mutants within the entire segment.

2. THE CONSTITUTION OF THE plexus blistered (px bl) STOCK

a. INTRODUCTION

The mutants described thus far originated repeatedly, directly or indirectly, from our so-called plexus blistered stock. We shall see later that after outcrossing this stock or its derivatives a considerable number of other mutants appeared. An explanation for the process of mutation in the material upon which this paper is based therefore requires a knowledge of the genetical condition of the basic px bl

stock, which will be analyzed in more detail than otherwise would appear necessary. Actually, our lack of knowledge of the spontaneous process of mutation is caused, in part at least, by neglect of details which do not seem to offer any new information to the geneticist and which are shoved aside as mere repetitions of well-known facts. Therefore we feel obliged to present many data which might otherwise be easily branded as elementary and not worth mentioning.

As was reported above, the px bl stock, the basis of the present analysis of mutation, contains the mutant locus plexus from a pure standard stock from which the px bl stock was derived. The blistering and high-grade plexation were obviously in part the additional effect of some bs (blistered) allele. Within the stock the amount of plexation and blistering varied, and the genetical situation revealed by selection as well as by crossing experiments was not a simple one. When analysis was attempted, it turned out that the phenotypes of different combinations not only overlapped, but also were influenced by different modifiers as well as by external conditions. The difficulty was increased when it was found that the bs stock used for test crosses contained another allele which produced certain compound effects phenotypically identical with others based upon a bs allele in the px bl stock. The disentangling of these relations required a detailed morphological study of the phenotypes found in px bl, in the plexation-producing tester stocks, and in the different compounds and combinations appearing in backcrosses. As the details furnish the information on the genetical constitution of px bl, data which in themselves are not pertinent to our problem will be presented as a part of the analysis.

The plexus blistered line (abbreviated px bl, without any genotypical meaning in these symbols), the origin of which from standard px was described above (see p. 293), has remained constant for many years, apart from the features already reported. This means that in mass culture as well as in closely inbred brother-sister cultures the same types were always found. There is, however, a definite variation, most easily recognized by the blistering of the wings, which characterizes the stock. For example, in one series of generations of the stock the number of blistered flies may be very high, and in another generation they may be almost absent in some bottles. The details of this variation exclude environmental influences as sole cause. Obviously, a genetic situation is present which changes its equilibrium in the mass cultures. But in the end the population is more or less the same. As an example I may mention the fact that some of my stocks threw a high percentage of blistered flies for many years, and with such constancy that I always had blistered flies available for experimentation. During the year 1940 all these stocks changed to very low incidence of blistering without any known change occurring in the external conditions, though the high-grade plexation remained. Two sets of selections were started by breeding from blistered females and, where possible, from blistered males also. In one of these lines the old condition of the stock was restored after three generations; in the other, selection succeeded in going beyond that, many of the males being also blistered (see below). Obviously, then, the main condition for blistering is homozygous in the stock, but additional modifiers needed for high incidence may be selected or counterselected. Actually, also, lines without any blisters at all, not distinguishable from px, have been selected. Other conditions of the stock became visible only after outcrossing, which varied in the stocks in the course of time, as will be discussed below.

b. DESCRIPTION

In general, this line may be described as typical high-grade plexus with more or less irregular occurrence of blisters upon the wing. A detailed analysis, however, shows the plexus formation not to be identical with that of the standard plexus mutant. As a matter of fact, the different laboratory lines of this mutant, though rather constant, are different from one another. It is not known whether different alleles or modifiers are involved. The lowest type known to me appears in a standard[9] combination with dumpy. This, however, is not due to a modifying action of dp, as a high plexation may be combined with dp and the low one separated from dumpy.

In the description, we shall use the following abbreviations and symbols (see plate 23), dispensing with the entomological terms. We mark the series of wing cells anterioposteriorly (called marginal, submarginal, first, second, third posterior cells) as I–V. An extra vein, or dot, or dash, or net, etc., in II means, therefore, a dash, etc., in the submarginal cell, etc. Correspondingly, we mark the longitudinal veins 1–5. A knot or an antler at 2 therefore means such a formation of extra veins attached to the second vein. The extra veins frequently unite with their point of attachment into a broad chitinous mass, sometimes strongly chitinized, sometimes not completely so. We call such a formation suggestive of a webfoot, a web. Cv is the posterior cross vein, to which extra veins or webs may be attached.

One of the most frequent extra veins is a dot, dash, or line in V, parallel to 5 near cv. It will be designated EV. If this EV elongates and finally forms a complete longitudinal vein, we call it a parallel vein. Frequently 4 and 5 branch off veins parallel to the wing margin. They may unite to form an arch vein or a periclinal vein.

The lowest px type shows only the following extra veins: a few branches of 2 into I toward the tip of the wing; a similar short branch from 2 into II; a short branch from cv into IV. A somewhat higher type of px, as isolated from a marked second chromosome stock, contains lines or net formation in I, sometimes dots in III. Frequently there is a dot or dash EV and a small antler formation attached to 5 near cv. A still higher plexus type, typified in a standard a px sp stock, is similar to the foregoing, but plus individuals have also more or less of the parallel vein in V and of the arch vein in IV. This last type corresponds with the original description of plexus in the Bridges-Morgan monograph (1919).

In the original plexus blistered line the lowest grades do not occur. The lowest type of plexation corresponds closely to the highest type in standard px as just described. But in numerous individuals a considerable web formation is attached to 5 near cv. More frequent is a higher type with a considerable web formation which unites the attachment of the arch vein to 5 with the attachment of the parallel vein in V. This web is broad and elongated. These two types, generally called low and medium plexus, are characteristic for populations with few individuals showing blistered wings.

In populations with much blistering a still higher type is prevalent (strong plexus). The web at 5 is extremely long and broad, arch vein and parallel vein are complete, and even branch into a network. The antler formations at 2 and 3 are also expanded into broad webs.

[9] "Standard"= derived from original Columbia and, later, Pasadena stocks.

Blistering may occur in these stocks, on one or both wings. The blister appears above the web at 5 and extends over a considerable part of the wing, more so when both wings are blistered. The blisters found in the lower plexus types at the same point, though more rare, are correspondingly less extreme. There exist still more extreme types of plexus formation which, however, do not occur in the pure px bl stock (see below).

The foregoing description applies to females. Males generally show the same types, but all features are less extreme; one might say they are one class below the female condition. Blisters are usually rare in the males, though lines with high incidence occur. The sex ratio is almost normal in the line (see below).

c. THE PHENOTYPE OF SECOND-CHROMOSOME MUTANTS AND DEFICIENCIES PRODUCING PLEXATION

Analysis of px bl requires a knowledge of the phenotypes of the tester mutants of a plexus-like type, which will be presented in this section.

Plexus (*px*).—The mutant px is available in lines with a different degree of phenotypic effect (see description below). No special inquiry has been made with respect to whether these represent multiple alleles or modifier effects. A low-grade plexus, as found in the px dp stock, does not show much extra venation. There is a posterior branch of the cross vein of different length; there is a dot, dash, or line in the marginal cell, and the third longitudinal vein carries posteriorly a more or less pronounced antler formation. Furthermore, the marginal ends of the veins are bent and sometimes branch into a delta. In the higher grades of px all these features are more strongly emphasized, the extra vein in the marginal cell becomes attached to the second longitudinal vein and forms branches, and a branch from the fifth longitudinal vein unites with a branch from the fourth vein, thus forming what we call the periclinal or arch vein. The attachment of the periclinal vein to the fifth longitudinal may become transformed into a network or a broad chitinous mass (web). In the third posterior cell a dot or dash appears. Plexus, which is registered as a recessive mutant, possesses a considerable amount of dominance. All crosses with wild type showed at least a dot or dash in the marginal cell in up to 75 per cent of the F_1 individuals. Whenever px enters into any heterozygous combination, this dominance effect will be found in a number of individuals and can be used as a marker. Plexus opposite a deficiency is not much exaggerated.

Blistered (*bs*).—The standard blistered (bs 107.3) which we received from Pasadena has remained rather constant in our cultures. The phenotype varies from perfectly normal flies through a series showing a small dot in the fifth posterior cell near the cross vein, to flies with a more or less long dash at this point, or a small antler-like structure more or less attached to the fifth longitudinal vein. We made frequent statistical checks of the conditions in stocks and pair cultures and found a certain fluctuation with a mean near the type of beginning antler formation. For crossing we always preferred the plus type with antler, which, as we shall see, was sometimes a compound of two bs alleles. Only once did we find a bs fly with plexus formation on the wing; the offspring, however, was not different from that of other flies. A pure bs fly with blisters on the wings, such as had been the type of the original mutant, was never found, and this at different external conditions, warm and cold. But we shall have to mention below certain bs alleles which produce a

definite type of blister. (These details are needed because this, like so many other stocks, no longer shows the characters given in the original description.) The bs of the line here used is, like px, an incomplete dominant; about 60 per cent of the heterozygotes with wild (Oregon) are normal, the rest varying from a small dot in the fifth cell to the complete antler. Whereas up to 20 per cent of normals were found in the pure bs broods, this means a considerable dominance. Once a single cross showed complete dominance of the antler in all individuals. (This was found prior to the discovery of the second allele and therefore was not tested for it.) The heterozygous dominance effects as well as the homozygous effects of bs and px are simply additive if present in the same individual.

Balloon (*ba*).—A third locus with a plexus effect is balloon (II.107.4). This locus was originally (see Bridges-Morgan monograph) supposed to produce a plexus effect with inflated wings. Among the stocks, all received from Columbia and later from Pasadena and in repeated sets, over many years, an individual was never found corresponding to the original description, whatever the external temperature. As a matter of fact, for years the balloon lines, which are supposed to be more conspicuous at lower temperatures, showed nothing but small and rare extra veins at whatsoever temperature and were practically useless. Some time ago, the same stock bottles bw ba sp kept in the same external conditions were found to contain exclusively a very distinct type which completely fits the original description but for the total absence of blisters under good conditions. (Blisters appear in old bottles when the flies become very small.) This type has since bred true irrespective of external conditions, and segregates typically from crosses. It is characterized by an extreme plexus formation which contains all the elements described for former combinations but with a somewhat different pattern. It shows in considerable degree all the elements of the plexus pattern. The antler formation in the fifth cell involves the whole end of the fifth longitudinal vein and is, in most cases, found as a broad chitinous mass. The periclinal vein is more or less complete, though nearer to the wing margin than in the former cases. The parallel vein is found in the plus individuals also. Near the ends of the third and fourth veins a considerable antler formation is found and long extra veins are located in the marginal cell (I), which is very characteristic. There is an inclination toward the formation of a network of extra veins in the submarginal (II) and third posterior cell (V) in the extreme plus individuals. The minus individuals show all these elements only slightly expressed.

We worked for some time with this balloon stock before strange crossover results suggested a check. (I emphasize again that at this time the stock had the phenotype as originally described.) Crossover tests with wild type as well as with marked stocks resulted in a practically free segregation of the plexus formation, considered to characterize ba, from bw, and sp, the last-named only 4 units from ba. An example of this is shown in table 78.

This indicated that the plexation, identical with the original phenotype, which had reappeared in the stock, was based upon a locus at the other end of the second chromosome. Therefore the locus net was suspected to be present in the stock. Crosses with the mutant net produced a plexus type different from both the net and the ba stock. From a cross with markers (as well as the one reported; table 78), individuals were isolated which showed the complete plexation without bw sp (see class 4 of table 78) and therefore were suspected to be the net crossovers. Crossed

to net, they produced all net flies, part of them blistered and part dark-colored. Actually, then, the change in the ba stock was the appearance of a net allele and its spread in the stock. The same net allele must have been present in the original stock. The compound tended to blistering (possibly based upon the additional presence of ba) and a constant net blistered stock was extracted. The dark color which appeared in one-fourth of the offspring from net × crossover net and of bw, sp, ba, and which was associated with rough eyes, stocky build, and bristle abnormalities, turned out to be an ebony allele. Further details do not belong here, but it ought to be mentioned as a remarkable fact that ebony was originally discovered in ba stock (by Miss Wallace) one of many similar instances which point to mutation as not a chance phenomenon.

The Plexates (Df(2)Px).—The fourth plexus-producing type which has been useful in analyzing the px bl stock is the Plexates. Bridges studied two deficiencies

TABLE 78

(bw sp ba × Ore) × bw sp ba

	♀	♂	
1. +	60	69	
2. bw sp ba	58	66	(as in stock)
3. bw sp	36	50	
4. ba (= px)	61	67	(as in bw sp ba stock)
5. bw	..	2	
6. sp ba	1	1	
7. bw ba	..	2	
8. sp	2	2	

involving the bs and ba loci, which he called Plexates because they produce a kind of plexus effect in heterozygous condition. They are lethal when homozygous. Px^2 is a deficiency for blistered and balloon, and Px^1 includes also speck.

The effect of Px^2 in heterozygous condition, $Px^2/+$, is not like one of the bs effects. There is a more or less pronounced antler formation in the third cell (V), varying from a little to a real antler formation. Also, there is a posterior branch to the cross vein and frequently a beginning of an antler formation attached to the third longitudinal vein in the submarginal cell. Moreover, extra veins are found in the marginal and the submarginal cell, which probably are the effect of the ba deficiency since ba heterozygotes show the same phenomenon (but in the presence of net/+) (see above). The compound Px^2/bs shows the expected exaggerated effect. All parts of the Px^2 pattern are more pronounced, and most individuals exhibit a part of the parallel vein as before. Sometimes a very small pearl-like blister appears on top of the broadened antler. But in some cultures all females have a considerable blister. Other types, based upon different alleles, will be described later. Males are not blistered. There is a certain range of variation and the sexual difference is encountered as always. (It has to be emphasized again that, in almost all combinations involving any type of plexus formation as well as blistering, the males exhibit a grade which in plus individuals nears the minus grades of females.)

Px^1 contains, according to Bridges, the speck locus besides bs and ba, as can be easily checked. It is a longer deficiency than Px^2. It is also lethal when homozygous.

TABLE 79

PHENOTYPES OF HOMOZYGOTES, HETEROZYGOTES, COMBINATIONS, AND COMPOUNDS INVOLVING WING PLEXATION

(The table gives the modal phenotype of females under conditions as nearly identical as possible and, where possible, from inbred lines. For explanation of abbreviations, see p. 404.)

Genotype	Extra venation in cell					Parallel vein	Peri-clinal vein	Antler web		Net in	Blistered		Ex-treme bl	Sack
	I	II	III	IV	V			At 5	Near cv		One wing	Both		
1. px/px −	+	+	..	+	..	..	..	..	..	..	..	..	..	..
2. px/px +	+	+	+	+	..	±	+	+	+	..	..	..	..	..
3. px/+	+	..	..	±	..	..	..	..	..	..	..	..	..	..
4. bs/bs	..	..	..	..	±	..	..	±	..	..	..	..	..	..
5. bs/+	..	..	..	..	±	..	..	±	..	..	..	..	..	..
6. bs^2/bs^2	..	..	..	..	..	..	..	..	++	II	..	..	..	..
7. ba/ba (incl. net)	+	+	..	+	..	±	+	+	+	I,II,V	..	..	..	..
8. ba/+	+	..	..	..	..	..	..	..	..	..	..	..	..	..
9. $Px^1/+$	+	+	..	+	..	..	..	+	+	..	..	..	..	..
10. $Px^2/+$	+	+	..	+	..	..	..	+	..	..	..	..	..	..
11. px bl stock	±	±	±	±	±	±	±	±	±	..	±	±	..	..
12. px bl/+	+	..	..	+	+	..	..	..	..	..	..	..	..	..
13. px +/+ bs = typ 3 + 5	..	..	..	..	..	..	..	..	..	..	..	..	..	..
14. px +/+ ba = type 3 + 8	..	..	..	..	..	..	..	..	..	..	..	..	..	..
15. bs +/+ ba = type 5 + 8	..	..	..	..	..	..	..	..	..	..	..	..	..	..
16. px +/+ Px^2 = type 3 + 10	..	..	..	..	..	..	..	..	..	..	..	..	..	..
17. bs/Px^2	+	..	..	..	..	±	..	±	±	..	±	..	..	..
18. bs/Px^1	+	+	..	+	..	+	+	+	+	..	+	..	..	..
19. ba/Px^2	+	+	..	+	+	+	+	..	+	I,II,V	+	..	..	..
20. ba/Px^1	+	+	..	+	+	+	+	..	+	I,II,V	+	+	..	..
21. px bl/px	±	±	±	±	..	±	±	±	±	..	..	..	..	..
22. px bl/bs	+	..	..	..	..	..	..	+	(+)	..	..	..	..	..
23. px bl/ba	+	..	..	+	+	..	..	..	..	..	..	..	..	..
24. px bl/Px^1	+	+	+	+	+	+	+	..	+	I, III	+	+	+	..
25. px bl/Px^2	+	+	+	+	+	+	+	..	+	I, III	+	+	±	..
26. Bld Def/+	+	+	..	+	..	±	+	+	+	I,II,V	..	..	..	..

TABLE 79—(*Continued*)

Genotype	Extra venation in cell					Parallel vein	Peri-clinal vein	Antler web		Net in	Blistered		Extrem bl	Sack
	I	II	III	IV	V			At 5	Near cv		One wing	Both		
27. Bld Def/px bl	..	..	..	..	..	..	..	..	..	..	..	..	..	Almost
28. Bld Def/bs	..	Like26	..	..	..	..	..	..	..	..	..	..	..	..
29. px bs/px bs = type 2 + 4	..	..	..	..	..	..	..	..	..	..	..	..	..	..
30. px ba/px ba = type 2 + 7	..	..	..	..	..	..	..	..	..	..	+	+	..	..
31. net	+	+	+	+	+	..	+	+	++	..	..	..	..	..
32. px bs^p/+ bs^p	..	..	..	..	..	..	..	..	+	..	..	..	..	..
33. px bs/+ Px^2	+	..	..	±	±	±	±	..	+	..	..	±	..	..
34. bs^p/Px^2	+	+	+	+	+	+	+	+	+	..	+	+	..	..
35. bs^2/bs	..	..	..	..	..	..	..	+	..	..	..	..	..	..
36. bs^2/px bs^p	+	+	..	..	..	..	..	+	..	II	..	..	..	..
37. px +/+ bs^2	+	..	..	+	±	..	..	..	..	..	..	..	..	..
38. bs^2/Px^2	..	..	..	..	..	..	..	..	..	..	..	..	..	+
39. bs^{bl}/px bl	..	..	..	..	..	..	..	..	+	..	..	..	..	..
40. bs^{bl}/Px^2	..	..	..	..	..	..	..	..	..	..	..	..	..	+
41. bs^{bl}/bs^{bl}	..	..	..	..	..	..	..	..	++	..	+	+	..	..
42. bs^{bl}/+	..	..	..	..	..	..	..	±	±	..	..	..	..	..
43. px bs^p/px +	±	±	..	±	..	±	±	+	..	..	..	..	..	..
44. px bs^{bl}/px +	±	±	..	±	..	±	±	±	±	..	..	..	..	..
45. px bs^p/px bs^p	±	±	..	±	..	±	±	±	±	..	±	..	..	..
46. px bs^p/px bs^{bl}	±	±	..	±	..	±	±	..	+	..	..	..	..	..
47. px bs^{bl}/px bs^{bl}	±	±	..	±	..	±	±	..	+	..	+	+	..	..
48. bs^{bl}/Blond Def almost lethal	..	..	..	..	..	..	..	..	..	..	..	..	+	..
49. bs^{pp}/+	..	±	..	..	±	..	..	..	..	..	..	..	..	..
50. bs^{pp}/bs^{pp}	..	..	..	..	..	..	..	..	..	..	..	..	betw	een
51. bs^{pp}/bs^{bl}	..	..	..	..	..	..	..	..	±	..	±	±	..	..
52. bs^{pp}/Px	..	..	..	..	..	..	..	..	..	..	..	..	..	+
53. bs^3/bs^3	..	net	..	..	..	..	net	..	++	..	+	+	..	..
54. bs^3/bs	..	..	..	..	..	..	..	±	..	..	..	..	..	..

Heterozygous $Px^1/+$ resembles $Px^2/+$ but has a somewhat stronger effect. The antler in the posterior third cell may be broadened to a chitinous mass, and the extra veins in the marginal and submarginal cell are better developed. The phenotypic action, then, corresponds to one of a higher allele.

The compound bs/Px^1, again, is similar to the one with Px^2 but is of a little higher grade; the blisters on top of the expanded antler are more frequent and a number of individuals have one wing really blistered.

Very typical are the compounds of ba (stock containing net) with the Plexates. ba/Px^2 shows the expected exaggeration effect for ba. This consists in a very strong expression of all the features of venation characterizing ba with net. It becomes especially visible in the extra veins of the submarginal and marginal cells, which form an extended and dense network; also in the third posterior cell the extra veins form nets. These characters are specific for the net containing ba, though their beginnings appear also in the bs series. One might actually describe these ba features as an extreme type of bs action, localized at certain points. Furthermore, many individuals of this compound are blistered. The compound ba/Px^1 is very similar, only still more extreme, and almost all females are blistered. This, again, is rather remarkable; ba separated from the net allele in our stock has no phenotypical effect and is useless, as stated before. But the exaggeration visible in the Px/ba compound is an exaggeration of the features produced by the net allele at the other end of the chromosome. This means that net acts not only as a producer of the net phenotype, but simultaneously as an enhancer for the otherwise subthreshold ba action. The exaggeration of the ba effect opposite a deficiency is simultaneously an exaggeration of the net effect located far away!

Here, then, as before, the combinations of a deficiency with bs and ba causing exaggeration of the plexation produce blistering as a part of more extreme plexation.

Blond (T(1, 2)Bld).—Another deficiency in this region which causes a plexus formation is Blond(2) deficiency, which removes the tip of II and thus is also deficient for sp bs and ba (but is duplicated for the tip of X). The plexus type is very similar to the one described for ba + net, but in addition the wings are spread though not blistered. This deficiency in compound with bs is not very much exaggerated, but is exaggerated with other bs alleles (see below).

All these types and some not mentioned, as well as those to be discussed in succeeding sections, are listed for easy reference in table 79.

d. THE px AND bs LOCI IN px bl

Crosses with bs and the Plexates.—As was stated before, the analysis has been complicated by the fact that standard bs is frequently heterozygous for a higher allele, called here bs^{b1}, which is very poorly viable in homozygous state and has a compound effect with bs within the range of variation of the bs phenotype. Also, some of the compounds involving the four alleles bs^{pp} and bs^{p} from px bl, and bs and bs^{b1} from bs stock, are phenotypically alike. This led to many detours. If px bl is crossed to bs/bs and px bl is from a balanced stock (to be described), namely, px bs^{pp} l/px bs^{p} $l^{1'}$ (l^1 being a lethal balancing bs^{p} against homozygous lethal deficiency l), F_1 segregates into the distinguishable though somewhat overlapping types, bs^{pp}/bs and b^{p}/bs. If px bl comes from a selected low stock lacking bs^{pp} and l as well as l^1, all F_1 are alike, that is, bs/bs^{p}. Both of the px bl types might also have

been crossed with a bs invisibly heterozygous for bs/bs^{bl}. In the first case, four types ought to appear in F_1, namely, bs^{pp}/bs, bs^{pp}/bs^{bl}, bs^{p}/bs, bs^{p}/bs^{bl}. With the low stock the segregation would be into bs^{p}/bs and bs^{p}/bs^{bl}. It was soon found that it is easier to distinguish the types obtained when the Plexates (1 and 2) are crossed into the stocks, which again led to analysis of the phenotypes produced in such crosses.

Table 80 contains some results of crosses px bl × bs. The stock px bl low (no. 11) is one in which the bs mutants had been selected out (px/px remaining). The pheno-

TABLE 80

PHENOTYPES OF F_1 FROM DIFFERENT px bl × bs

No.	Cross	♀		♂		Only EV, no antler	
		± antler	antler and web	± antler	antler and web	♀	♂
837	px bl × bs	54	..	37	..	..	..
844	px bl × bs	15	..	8	..	..	..
845	px bl × bs	88	..	29	..	..	..
857	px bl × bs	85	..	39	..	..	..
841	px bl blist × bs	50	..	22	..	..	..
834	bs × px bl	46	..	..	..	..	33
833	bs × px bl	..	..	..	..	47	45
835	bs × px bl	..	..	..	..	48	37
847	px bl low × bs	..	..	..	..	59	44
851	bs × px bl low	..	..	..	..	42	23
852	bs × px bl low	..	..	..	..	27	43
838	px bl × bs	15	31	22	7	..	..
843	px bl × bs	29	23	25	3	..	..
854	px bl × bs	11	11	4	4	..	..
855	px bl × bs	51	43	16	15	..	..
638	px bl × bs	22	34	20	24	..	..
639	px bl × bs	9	15	12	12	..	..
641	px bl × bs	1	12	3	1	..	..
642	px bl × bs	44	31	20	24	..	..
840	px bl blist × bs	29	21	22	11	..	..
846	px bl low × bs	40	15	..	..	..	39
849	px bl low × bs	8	9	..	..	..	35
853	bs × px bl low	18	17	..	..	..	34

types EV antler, web have been explained above. The table shows four types of F_1 results: (1) no segregation, and both sexes with antler near the cross vein; (2) no segregation, but both sexes of a lower type; one cross, 834, combines both types in the ♀♀ and ♂♂, respectively; (3) segregation into ½ antler, ½ web in both sexes; (4) the same segregation in ♀♀, but all ♂♂ low. Nos. 2 and 4 occurred six out of eight times when px bl low was involved. These results agree with the assumption that most of the parents from px bl were heterozygous bs^{pp}/bs^{p}, which produces with bs the compounds bs^{pp}/bs = web and bs^{p}/bs = antler (group 3). A number (group 1) had been bs^{p}/bs^{p}, and F_1 was uniformly antler (once the expressivity was lower in the males and twice in both sexes). Selected px bl low = px without bs gave with bs only the bs/+ effect = group 3. Only in group 4 was the bs parent obviously heterozygous for bs^{bl}. By chance, no combination $bs^{pp}/bs^{p} \times bs/bs^{bl}$ was made, which

would have been easily recognized because Df/bs^{b1} is a very extreme type called "almost sac" (see below).

We tried to prove these formulations by F_2 and backcrosses breeding from the different F_1 types. The results agreed with expectation, but for more transgressing variation toward EA and +, probably resulting from recombination of modifiers when the F_1 bs or antler types were bred. But when the web types from F_1 were bred, the segregation was such that no classification came near the simple expected ratios. Of course web might have been either bs^{pp}/bs or bs^{b1}/bs^{p} (and, in addition,

TABLE 81

px bl DIFFERENT TYPES × Cy/Px^2

No.	px bl mother type	Phenotype F_1 (not Cy)
2497	PV, EV.....	EV. Only a few PV. Many ♀ few ♂ blist. No segregation visible
2498	PV, EV.....	EV. Only a few PV. Many ♀ few ♂ blist. No segregation visible
2499	PV, EV.....	Both sexes about ½ blist, otherwise as before
2501	PV, EV, bl.....	Like 2497
2502	PV, EV, bl.....	Like 2497
2503	PV, EV, bl.....	Like 2499
2513	PV, Pa V, W.....	Like 2497
2504	PV, Pa V± bl.....	Like 2499, but more PV
2505	PV, Pa V± bl.....	Clear segregation of two types ♀ and ♂: ½ as before with or without blisters, ½ with extreme types of all veins and both wings extremely blistered
2507	PV:px, Pa V±, W..	Like 2505
2508	PV:px, Pa V±, W..	Like 2505
2509	PV:px, Pa V±, W..	Like 2505
2510	PV, Pa V, W, bl....	Like 2505
2514	PV, Pa V, W, bl....	Like 2505
2512	PV, Pa V, W, bl N..	All ♀♂ of the extreme type as before

Legend: PV = periclinal vein
EV = Extra vein, third posterior cell
bl = blistered
Pa V = Parallel vein (− = minus type, + = plus type, no sign = complete)
px = Much plexus formation in cells
W = web-like broadening where V, cross vein, and Pa V join
N = net formation at 5th vein
(The other constant features of px bl, such as extra veins in I, antler at 3, not marked)

bs^{pp} and bs^{p} were or were not linked with lethals), but even then the results could not have been classified clearly. Hence we resorted to introducing the Plexates because the exaggeration effect of these deficiencies would produce clearer differences between the classes. On this occasion the presence of bs^{b1} was discovered, since bs^{b1}/Px shows the extreme type sac.

We must first find the phenotypes of the possible compounds. Those of + or bs/Px^1 or Px^2 have been described above. In crossing px bl from nonselected stock with the Plexates, we realize that px bl may be the balanced individuals bs^{pp} l/bs^{p} l^{+}, or bs^{p}/bs^{p}. Actually, these can be distinguished phenotypically, as will be shown below, though there is a certain amount of transgression. The more extreme plexation and blistering indicate the compound with the high allele (plus homozygous px); the less extreme grades lack this allele. Table 81 reports upon the phenotypes of a series of crosses of females px bl, taken simultaneously from an inbred stock, with Cy/Px^2

males. Only the major features of the phenotypes of P and F_1 have been recorded. In analyzing this table it must be kept in mind that px/px × Px^2 shows nothing but the ordinary heterozygous effects of both. Everything beyond this (see description, p. 409) is at least the additional effect of the exaggerated bs locus in px bl. The px bl females which were crossed were different in the details indicated in the table. In a general way, we have a lower group without much parallel vein (which is an increased EV) and with maximally an antler formation in the third cell near the cross vein. In the second higher group this is replaced by a fairly large, web-like structure. The parallel vein increases in length. One extreme individual (2512) has also a net formation in different cells. The F_1 results correspond very closely to this grouping, with one overlapping case (no. 2505). The first group of females produces a lower type of F_1 compound. The EV or antler is exaggerated to a web (less so in males, as always); there is a considerable plexus formation in the second cell,

TABLE 82

BLISTERING IN px × Px_2

♀		♂	
not blist	blist	not blist	blist
4	12	16	2
4	30	3	17
6	35	13	16
18	11	31	2

and a varying number of blistered individuals, usually more females than males. But sometimes rather exactly ½ of both sexes are blistered. The blistered or not blistered condition of the mother obviously has nothing to do with the F_1 blistering, which we found also in other compounds with Px^2.

In this table the somewhat varying percentage of blistering has not been recorded in detail. However, this was done in some other crosses and a few examples are listed in table 82. Obviously, the mother was bs^p/bs^p, and the type described for F_1 is bs^p/Px^2 (plus px/+). It is much more plexated and blistered than bs/Px^2, thus indicating that bs^p is a higher allele.

The second, higher plexus group of px bl mothers produces a clear segregation into ½ females and males as before, blistered or not blistered, blistered meaning a small blister above the web in one of the wings, not the type of extensive blister present in the px bl line. The other half consists of females and males with an extreme plexus formation, i.e., all the elements in their maximal expression and, in addition, both wings heavily blistered. There is, finally, the very extreme mother of the cross 2512 which produced offspring exclusively of the last extreme type!

This looks as if px bl of the higher type had been heterozygous for two different bs alleles. It is hardly to be expected that one of them was a deficiency, as a viable homozygous deficiency of such size is very improbable. Otherwise, there was no evidence of a lethal class (Cy : not Cy = 2 : 1), but this might be meaningless because the Cy class was always much smaller in this series.[10] The test would be to backcross the different types to Px^2. Many reciprocal backcrosses to Px^2/Cy were therefore

[10] We shall return, below, to this point when discussing the visible deficiency linked with bs^{pp}.

made. As the Px^2 deficiency is lethal when homozygous, the backcross can yield only the parental F_1 type in the not Cy class, provided only the second chromosome is involved. Table 83 presents the results.

TABLE 83

HEREDITY OF TYPES OF PLEXATION

No.	Cross	F_1	RF_2
2553	Px^2 × 2504 type (not blist)	all low (blist or not)	♀ ½ like F_1, ½ extreme
2555	Px^2 × 2499 type (not blist)	all low (blist or not)	½ like F_1, ½ very low-grade px
2558	Px^2 × 2498 type	all low (blist or not)	Like F_1 but mostly blist
2563	Px^2 × 2513 type	all low (blist or not)	Like F_1
2564	Px^2 × 2502 blist	all low (blist or not)	Like F_1
2577	Px^2 × 2497 blist	all low (blist or not)	Like F_1
2565	2499 blist × Px^2	all low (blist or not)	Like F_1
2569	2498 blist + × Px^2	all low (blist or not)	Like F_1
2570	2502 type × Px^2	all low (blist or not)	Like F_1
2571	2497 blist + × Px^2	all low (blist or not)	Like F_1
2573	2502 extr × Px^2	all low (blist or not)	♀ about ⅓ extr, ♂ only few extr
2575	2513 blist − × Px^2	all low (blist or not)	Like F_1
2591	2497 blist + × Px^2	all low (blist or not)	½ like F_1, ½ very low grade
2597	2503 blist − × Px^2	all low (blist or not)	½ like F_1, ½ very low grade
2599	2498 blist − × Px^2	all low (blist or not)	Like F_1
2596	2503 blist − × Px^2	all low (blist or not)	Almost all very low-grade px
2559	Px^2 × 2505 low	½ low, ½ extr	Like father
2562	Px^2 × 2505 low	½ low, ½ extr	Like father
2579	Px^2 × 2514 extr	½ low, ½ extr	♀ ½ extr, ½ not; ♂ extr px but not blist (like ½ ♀)
2580	Px^2 × 2507 extr	½ low, ½ extr	♀ ½ extr, ½ not; ♂ extr px but not blist (like ½ ♀)
2581	Px^2 × 2505 extr	½ low, ½ extr	♀ 2 not extr: 1 extr, ♂ extr px but not blist (like ½ ♀)
2568	2505 low blist − × Px^2	½ low, ½ extr	Like mother
2574	2508 extr × Px^2	½ low, ½ extr	[a]Many both wings blist, no extremes
2582	2507 extr × Px^2	½ low, ½ extr	♀ 2 not extr: 1 extr, ♂ not extr
2584	2507 extr × Px^2	½ low, ½ extr	♀ ½ extr, ♂ only few
2585	2507 extr × Px^2	½ low, ½ extr	♀ only few extr, ♂ all low[a]
2587	2507 extr × Px^2	½ low, ½ extr	About ⅓ extr[a]
2588	2507 extr × Px^2	½ low, ½ extr	♀ about ⅓ extr, ♂ only few[a]
2589	2505 extr × Px^2	½ low, ½ extr	♀ about ⅓ extr, ♂ only few[a]
2590	2505 extr × Px^2	½ low, ½ extr	♀ about ¼ extr, ♂ none, and some very low[a]
2594	2505 extr × Px^2	½ low, ½ extr	♀ about ¼ extr, ♂ a few[a]
2595	2505 extr × Px^2	½ low, ½ extr	♀ about ¼ extr, ♂ a few[a]
2598	2514 extr × Px^2	½ low, ½ extr	♀ about ¼ extr, ♂ a few[a]
2572	2512 extr × Px^2	All extr	♀ only few extr, ♂ none (small numbers)

[a] In these broods the mothers probably were not virgins, the ratios are therefore not relevant.

This table shows at once that something besides the second chromosome is involved in the F_1. A number of the R F_2 resemble F_1, showing that here only the bs locus from px bl was involved, producing an exaggeration with the deficiency, the plexus, and partly blistered type, as described. But there are also a few different results. Three times (nos. 2555, 91, 97) only one-half of the individuals were like

the F_1; the other half show only an extra vein and a branch at a cross vein and a short extra vein in I or II, these together being the type of plexation found in px bl × wild or in Px/+. A few individuals of this type occurred also in other cases. It turned out that these were Cy/Px^1 flies in which Cy did not show phenotypically.

Still more unexpected is the case of 2553, where one-half of the R F_2 females (only one male) show the extreme blistered type not present in F_1. This indicates that a recombination with another chromosome containing an enhancer is responsible for this type. The same is borne out by the crosses involving the extreme type. The latter never bred true, as it ought to if it is based upon the bs locus alone, but segregated into extremes and not extremes, the latter being high-grade plexus but not blistered. The ratios which occur in the females are either 1 not extreme : 1 extreme or 2 not extreme : 1 extreme. Looking over these crosses, we realize further that no extreme males and few females are produced when the father is the F_1 male, i.e., the X chromosome of the R F_2 male is derived from Px^2 stock. However, extreme males

TABLE 84

(px bl × Px_2)²

No.	♀			♂			
	px⁺ blist	extr px bl	± web	px	px bl	extr px bl	antler-web
2670–71, 2323–26.	229	281	12	247	119	85	24

do appear in the reciprocal cross, though in small numbers. It is possibly the X chromosome from px bl which is responsible for this effect, and the females may be heterozygous or homozygous for the condition. But it is also possible that a dominant condition at the other end of the second chromosome is responsible and is removed in F R_2 from bs by crossing over.

But one difficulty still remains: cross 2553, where one-half extreme offspring was sired by a low male from low F_1, which is supposed to have had neither the X chromosome with the condition for extreme blistering nor the assumed second-chromosome condition. No interpretation can be offered. The whole situation does not lend itself to a simple interpretation, beyond the statement that other loci are involved.

We assumed that in all these cases only bs^p was present, because bs^{pp} is associated with a deficiency inside Px^2. However, even if Px^2/bs^{pp} Df were viable and the extreme type, the result would not be any clearer. It may be added, finally, that in the bs situation, whatever it is, no other neighboring loci were involved. Many were tested but gave negative results, as has already been reported for one of them, namely, balloon. Thus we come to the conclusion that the bs^p allele in px bl is a higher allele of bs and that its effects are subject to considerable enhancement by modifiers in other chromosomes.

The phenotypes of bs^p homozygous without px/px could be found by crossing over between px and bs, which simultaneously removed the lethal linked in the original stock with bs^p. The clearest case was obtained in a set of crosses which did not contain the lethal in the bs^p chromosome. In F_1 px bl × Px^2, extreme plexus and completely blistered flies bs^p/Px^2 were obtained. F_2 from these gave the results

shown in table 84. Considering the overlapping between the extreme and less extreme classes, and the ever-present shift toward the lower type in males, this represents the segregation into two Px_2/bs^p = extreme, one bs^p px/bs^p px = plexus ± blistered and crossover bs^p px/bs^p. The latter, web without px in females and a little lower type (antler web) in males, is the type of homozygous bs^p. The extracted types bred to expectation. The phenotype thus obtained assigns bs^p to a position between bs and Bridges's bs^3.

When stock bs^2 was first received from Pasadena, it showed an extreme web formation where the antler is situated in bs, and a fine net formation in II. Later the type changed, showing a range of variability from EV up to the type just described. Blisters were never observed above the web. But later they again appeared in the stock and seem to be dependent upon the moisture conditions. The original phenotype, then, was a little higher than the type bs^p/bs^p isolated from px bl stock. The compound bs/bs^2 is not very different from a plus condition of bs, showing that no deficiency and no dominance are involved. The compound with px bl, i.e., bs^p/bs^2, is different from px bs^p/bs. Besides the antler (±) there are extra veins in I and II, the latter sometimes forming a net, and a branch to the cross vein. The effect of px in this case is not large, as the combination px +/+ bs^2 shows only the usual extra vein in I, a branch to the cross vein, and the heterozygous bs condition from + to EV. Most characteristic is the compound bs^2/Px^2. Here the usual exaggeration effect of the deficiency produces structureless, inflated, shortened and narrowed wings carried in a spread condition, a type which we call sac.

We have already stated that our standard bs stock contained in irregular distribution another bs allele which we call bs^{b1} and which is a still higher allele than bs^2 of low viability and fertility. In reporting the px bl × bs crosses (see table 80) we mentioned that in some cases all F_1 individuals showed the antler at CV, being the effect of the compound bs^p/bs. In other cases one-half of the F_1 individuals were as described, the other half showed an exaggerated antler with web formation, a type of exaggerated bs action which we described for other compounds. The cross was afterward repeated many times. Sometimes a whole series never produced the exaggerated type; sometimes many or even the majority of crosses gave 50 per cent offspring of the exaggerated type. Never were all flies of this type. As the bs stock is usually responsible for the result, something is present there which fluctuates in numbers in the stock bottles and is either lethal or too unviable to appear in homozygous condition in the stock bottles. It turned out that the classification of F_2 and backcrosses was very difficult on account of considerable overlapping in the presence of px, and therefore the exaggeration effect of the Px^2 deficiency was again used for further tests. F_1 web individuals were crossed to the Plexates, the nonweb F_1 crossed to the same (already reported) serving as controls. This cross (px bl × bs) web × Px^2/Cy ought to yield, apart from the Cy half, one-half of the already analyzed px bl/Px^2 compound and one-half of the supposed higher bs allele (bs^{b1}) opposite the deficiency. The latter would be recognized by the exaggeration effect, which has already been described for bs, bs^p, and bs^3. Actually, one-half of the offspring from this cross showed the type sac just described for the bs^2/Px^2 compound. The test was provided by either crossing many bs with Px^2 or with (bs × +) × Px^2, in which case sac segregated whenever bs was heterozygous for bs^{b1}. Homozygous bs^{b1} was then to segregate from sac parents = $bs^{b1}/Px^2 \times bs^{b1}/Px^2$ as one-third of the

offspring. An actual result from 17 such F_2 was 836 females 797 males sac, 196 females 164 males bs^{bl}/bs^{bl}, showing the latter type rather unviable (about 50 per cent viability). Individual ratios are frequently very low, e.g., 16 : 1 instead of 2 : 1.

The segregating type bs^{bl}/bs^{bl} is very characteristic: it has a very extended web near the cross vein which reaches the edge of the wing. Above this web a blister is formed which is present in one or both wings. The type then closely resembles Bridges's bs^2, but is more extreme, a condition which is expressed in its low viability and considerable sterility. Many flies do not produce offspring, and those that do produce only few individuals. A stock could not be kept up for many generations, even with large numbers of parents used.

The stock bs^{bl}/Px^2 = sac derived from $bs \times Px^2$ thus was phenotypically identical with one, also sac, derived from (px bl × bs) type web × Px^2. But it soon became clear that the two stocks were only phenotypically alike. In the stock not involving px bl, later tests always gave the expected results for sac = bs^{bl}/Px^2. Sac × sac segregated bs^{bl}/bs^{bl} in less than one-third of the offspring, which bred true if at all. Further $bs^{bl}/bs^{bl} \times Px^2$ gave only sac. We made the same tests with the sac derived from (px bl × bs) × Px^2 by breeding from sac flies (in mass because of low fertility and viability), and again the offspring always segregated in sac and the high web type; the latter type crossed with Px^2 produced only sac. But pairs of the high type resembling bs^{bl}/bs^{bl} only occasionally bred true; sometimes they segregated sac. We shall return to this strange result at once. Actually, this stock, which was always bred from numerous sac flies, changed after a long series of generations of typical behavior. The segregating homozygotes were now of a lower type, about like bs^2. These had now become perfectly fertile and they bred true. The new type was rather different from the former extracted homozygotes. The web did not reach the wing margin, but there was more or less of a parallel vein present; the wings were blistered, or not. Males were never blistered, though they were so in the extracted homozygotes. Crossed with the Plexates, they still produced sac. But, in addition, the sac type also had changed to something between extreme plexus blistered and sac, i.e., a little wing structure was left.

The clue to these incongruities was found when many of the bs^{bl}/bs^{bl} type flies derived from the cross involving px bl via sac were tested before these changes occurred. As has already been reported, many of these tests (checked over and over again for virginity because of the incongruous breeding behavior) produced both their own type and sac from both parents of the high web type, and were, besides, more fertile and viable. Among three of these segregating broods were a few bs^{bl} type flies with additional plexus, obviously crossovers, which required the presence of a px containing chromosome from px bl stock in the parents. A pair of such flies found in the stock bred true and was much more fertile than usual and also viable (2414). Obviously, this stock, which was supposed to be bs^{bl}/Px (sac) segregating bs^{bl}/bs^{bl}, contained an admixture of a compound of Px with another second chromosome from px bl carrying a different bs allele, namely what we previously called bs^{pp} present together with px, i.e., bs^{pp} px/Px. We have already seen that bs^{pp} px homozygous is almost sac. As we had made up the stock by mass breeding on account of unviability of sac and bs^{bl}, by chance bs^{pp} had also entered the stock derived from (px bl × bs/bs^{bl}) × Px. Thus, among the phenotypes sac of this stock there were mostly bs^{bl}/Px and some bs^{pp}px/bs^{pp}px flies; the latter were a minority and

by chance this type was never used alone for breeding, which was always done with a few pairs of sac (bs^{pp}/Px^{s} is also sac). The phenotype bs^{bl} in the stock thus was either bs^{bl}/bs^{bl} or $bs^{pp}px/bs^{bl}$, and by crossing over $bs^{pp}px/bs^{bl}px$ could also be obtained. A cross $bs^{pp}/bs^{bl} \times bs^{bl}/bs^{bl}$ seemed to breed true; though the lower grade web of the bs^{pp}/bs^{bl} flies and their better breeding was noticed. A cross $bs^{pp}/bs^{bl} \times bs^{pp}/bs^{bl}$ segregated the almost sac flies, which now bred true. Extracted F_3 agreed with these interpretations. Finally, the change which later occurred in the stock, as described, consisted first of a spreading by selection of the viable bs^{bl}/bs^{pp} type, which seemed to breed true, and the spreading of the bs^{pp} homozygous almost sac type. But there is a considerable selection against sac, bs^{pp} and bs^{bl}, as compared with the best viable bs^{bl}/bs^{pp}, which actually were predominant when last tested, whereas bs^{bl}/bs^{bl} (similar phenotype) had been very rare in the original stock.

Table 79, as already stated, contains an evaluation of the average phenotype of different combinations and compounds, among them a number not mentioned in the text. The description applies to nonisogenic stocks kept under more or less identical conditions. There is much variability and overlapping, as mentioned in the text, and there are modifiers, which have been traced, that increase or decrease the average extravenation. On the whole, however, the table gives a fair description of the types found in such actual experiments where a clear classification was possible.

It might finally be added that the degree of plexation produced by the px bs combination in px bl can be considerably enhanced by the presence of the Payne inversions in the third chromosome. This was noticed when test crosses were made with the dominant Sb (Stubble) associated with such an inversion, or not. The former produced exaggeration of px, the latter did not. The dominant S (Star) is known to act as a suppressor of plexation. The same was found for H (Hairless) in some crosses.

Remarks on the phenogenetics of plexation.—Though it does not actually belong to the problems of this paper, a short discussion of the phenogenetic features involved in the foregoing analysis of the plexus wing types may be added.

Looking over all the phenotypes recorded in these different heterozygotes and compounds, we realize that they all more or less obey a definite rule. Let us consider first the bs series, namely, bs, bs^{p}, bs^{bl}, bs^{s}, bs^{pp}, and their compounds, including the compounds with the Plexates. The lowest action of bs upon the wing is not visible, i.e., the wing is normal. The seriation of visible effects is perfectly orderly in the homozygotes, heterozygotes, and compounds, namely, a simple addition of the effects of each locus, within the range of a certain fluctuation. To this is added the perfectly orderly effect of the exaggerating deficiencies, orderly so far as the exaggeration parallels the series of the effects of the respective alleles opposite the deficiency. The order of the effects is: dot, dash, antler, large antler in V; broadening of the center of the antler into a web; large web, extreme web extending to wing margin, beginning blister above the web in one wing, both wings, considerable blistering, extreme blistered wing, almost sac and sac wing. Normally, the effect is then confined to the cell V, though occasionally other extra veins occur even in the absence of px/+. If the exaggerating deficiency is present, the action of this compound spreads to the other wing cells and the complete series of effects characterizing the px and ba action is found, again in their proper order of increase in the respective compounds.

The plexus (and ba) series is also an orderly one in homozygotes, heterozygotes, and compounds of px, and in exaggerated conditions produced by the simultaneous presence of mutation or deficiency at the bs locus, or modifiers of a different kind. The pattern for the px action is a different one from that for bs. It begins with extra veins in I, II, and IV, and only in the higher grades do the same elements appear as in the bs series in V. The seriation is, roughly: extra veins in I; in I and IV; in I, II, and IV; ± periclinal vein, ± parallel vein and antler and web formation, in II and V. In a general way, we may say that the action of bs and px is similar, but the first starts at the posterior part of the wing and proceeds there to a high grade before other parts are affected; px, however, starts at the anterior edge and in cell IV and spreads to the posterior part of the wing in the higher grades. If both mutant loci are present, they are additive; heterozygous loci, too, have an additive effect. The deficiencies at the bs and ba locus act upon both series of effects in a similar way.

It may be added that still other patterns exist. The mutant net (left end of second chromosome) shows a series strongly resembling the px series combined with the bs series. But here the antler formation at the fifth longitudinal vein is pushed still more toward the wing edge, where it extends toward the fourth vein and tends to supplant the periclinal vein by a broad mass of chitin near the wing edge, whereas the other extra veins do not increase considerably. There is an additional tendency toward net formation in the submarginal cell from the antler of the third vein.

One of the most important facts known for certain series of multiple alleles is that the genic effect takes place at different times in development, namely, progressively earlier the higher the alleles (details and literature in Goldschmidt, 1938). It would be interesting, therefore, to relate the series discussed here to developmental facts. A complete analysis of the development is not yet available. But a few facts are already known (see Waddington, 1940, and photographs in Goldschmidt, 1935*a*). In normal wing development in the pupa the third and fourth longitudinal veins are ahead in differentiation. The second vein is rather late, and the fifth lags far behind. The part of the fifth behind the cross vein is perfected latest of all. At the time when the third and fourth veins are clearly visible, the region of the fifth and of the cross vein is still a wide-open sinus. And even when most of the veins have reached their final shape the cross vein and the fifth are wide channels (see photographs in Goldschmidt, 1935*a*). Extra veins which become visible only late in development must be formed by incomplete concrescence of the wing membranes. If such a disturbance happens, its first indications ought to be where the regular veins are last perfected. This is the region of the third posterior cell (V) and of the cross vein. What little information is available thus far seems to indicate that in the bs series as well the low grades are produced by action late in development and the higher grades by earlier incidence of the disturbance.

We add only that blister formation is the consequence of very incomplete concrescence of the wing membranes, allowing the blood which is pressed into the wing at eclosion to enter between. The actual series of blistering agrees with the expectations on a time basis. At present this is as far as we can go. A detailed discussion might be useful after Waddington, who recently published a preliminary account of the development of venation, has presented the details. As the difference between the px and bs effects is mainly one of pattern, i.e., the start of the process at the

anterior and posterior edge of the wing, respectively, it might be pointed out that a similar difference exists for the vestigial and Beaded type of scalloping of the wing. In this case, Braun (1940) was able to show that the type can be shifted to one of the other pattern by changing the speed of larval development. It might be added, finally, that wing plexation can be produced in wild type by temperature action in a critical period as a so-called phenocopy (see Goldschmidt, 1935), just as is the case with other mutants already discussed. This shows that most interesting phenogenetic facts are here at hand which deserve further analysis, the more so when we add that the degree of plexation is enhanced by the same inversions which also enhance the degree of scalloping (see Gardner, 1942, and Goldschmidt and Gardner, 1942).

e. BLISTERING IN THE px bl STOCK

One of the characteristic features of the original px bl stock which remained constant for years in some of the stocks (without selection) was the regular incidence

TABLE 85

BLISTERING IN px bl BROODS

No.	♀	♀ blist	♂	♀ both wings	♂ blist	♀ : ♀ blist
4019 B	35	39	50	..	..	0.9 : 1
4020 B	58	51	123	9	3	1.0 : 1
4021 B	38	49	105	2	..	0.7 : 1
4027 B	54	28	80	3	..	1.7 : 1
4028 B	63	45	104	..	2	1.4 : 1
4059 B	58	6	39	..	..	9.7 : 1
4060 B	62	16	87	..	1	3.6 : 1
4075 B	63	20	77	4	2	2.6 : 1
4077 B	68	22	98	..	..	3.1 : 1
4089 B	5	30	25	1	..	0.2 : 1
4090 B	63	29	95	3	..	2.0 : 1
4091 B	5	11	20	2	..	0.5 : 1
4096 B	27	19	70	2	..	1.3 : 1
4097 B	61	34	84	2	2	1.7 : 1
4099 B	24	30	45	4	..	0.7 : 1

of blisters, usually upon only one wing, in a high percentage of females and in only a few males. As the bs locus is involved, this blistering might be the phenotype of the bs homozygote or compound combined with homozygous px. The presence of blisters in only a part of the females and rarely in males would agree with the phenotypic effect found in some compounds with the Plexate deficiencies, as described above. The selection experiments within the stock (see below) might agree with such a simple interpretation, but the outcrossing experiments show it to be wrong.

Blistering within the original px bl stock.—One of the most conspicuous features of this line is the blistering of the wings. As a rule, only females are blistered and only one wing is blistered. When the incidence of blistering is high, females with both wings blistered, and blistered males, appear. The following experiments performed within the px bl line soon after it was found show that this blistering has a genetic basis and not a simple one. (The stocks have changed meanwhile; see below.)

In an experiment which involved breeding from different types of pairs over six

generations, females with one or both wings blistered and males with blisters were obtained (px and px blist describe only the phenotype, not the loci). The total numbers are given in table 85. This table shows that from all combinations a rather constant percentage of females with both wings blistered and blistered males were produced, namely, around 1.3–1.4 per cent. The double-blistered females and the blistered males appear in equal percentages and therefore are possibly due to the same genetic situation, actually a small overlap of incomplete penetrance.

TABLE 86

FEMALES WITH BOTH WINGS BLISTERED, AND BLISTERED MALES IN DIFFERENT px bl COMBINATIONS

Combination of parents	♀px	♀px blist	♂ px	♀both wings blist	♂ blist	♀ both wings blist		♂ blist per cent of ♂	Per cent ♀ blist one wing
						Per cent of all ♀	Per cent of blist ♀		
♀ ♂ not blist...	3142	1181	4223	72	42	1.7	6.1	1.0	39.0
♀ blist ♂ not...	2703	1191	3577	48	50	1.3	4.0	1.4	44.0
♀ and ♂ blist...	1402	556	1778	20	34	1.0	3.4	1.9	39.6
♀ not ♂ blist...	337	129	489	4	7	0.9	3.1	1.4	38.3
	7584	3057	10067	144	133	1.4	4.7	1.3	40.3

Many tests were made to find out whether the percentage of blistered individuals has a genetic basis beyond the homozygous bs^p locus together with px/px. External conditions may act to a certain extent in influencing the percentage, but the average production of blistered flies is independent of external conditions. Fifteen pairs of females and males without blisters gave offspring as listed in table 85.

This group shows a considerable diversity which might be more than fluctuation. The statistical tests show for an assumption of 40 per cent blistered as found in the grand total (table 86) a $\chi^2=0.98$ $P>0.30$; but the homogeneity test is negative, i.e., $\chi^2=119.42$ $P<0.01$. Thus the ratios are not significantly different from those found in table 86, but the series is probably not homogenous. From these broods the following selections were made:

1) Selecting from bottle 4059 with only 1/10 blistered flies, we got:

♀♂ not blistered, 4059:
No. 4222 13 ♀ 4 ♀ bl 13 ♂
No. 4223 104 ♀ 21 ♀ bl 173 ♂

which is a rather low ratio for blistered, indicating a genetic basis.

F_3 from not blistered, 4223, gave:
No. 4389 53 ♀ 12 ♀ blist. 67 ♂, which again is a low ratio.
F_4 from not blistered, 4389, gave:
No. 4539 38 ♀ 14 ♀ blistered 45 ♂

2) Selecting normals from bottles with a 1 : 1 ratio in the first generation, we found:

No. 4132 ♀♂ normal no. 4019: 80 ♀ 30 ♀ blist 104 ♂
No. 4133 ♀♂ normal no. 4019: 75 ♀ 91 ♀ blist 116 ♂
No. 4185 ♀♂ normal no. 4099: 94 ♀ 50 ♀ blist 126 ♂

which looks like the same ratios as were found before in the whole group.

F_3 from the last out of normals:
No. 4371 42 ♀ 16 ♀ blist 61 ♂, a rather low ratio

3) For normals selected from bottles with an intermediate ratio (namely, 4060) see table 87. All these selected F_2 from an F_1 showing a 3 : 1 ratio gave a very low ratio, namely about 8 : 1.

TABLE 87

SELECTION IN px bl

No.	♀	♀ blist	♂
4224 B	98	9	117
4225 B	106	8	97
4226 B	101	13	105
4227 B	93	15	104
4228 B	76	10	85
Total	474	55	508

In F_2 and F_3 of this set of selections, then, the same ratios reappeared as were found in the first generation, namely, high, medium, and low, and there was some effect of selection for low percentage of blisters.

TABLE 88

SELECTION IN px bl

blist ♀ from no.	Ratio F_1 ca.	No. F^2	♀	♀ blist	♂	
4021	1 : 1	4124 B	51	31	92	
4021	1 : 1	4125 B	51	48	102	
4021	1 : 1	4126 B	113	51	153	
4021	1 : 1	4127 B	80	26	126	
4021	1 : 1	4128 B	68	36	108	Mother both wings blistered
4020	1 : 1	4129 B	40	17	70	
4020	1 : 1	4131 B	81	32	87	
4019	1 : 1	4134 B	89	33	120	
4019	1 : 1	4135 B	94	28	105	
4019	1 : 1	4136 B	55	14	76	
4019	1 : 1	4137 B	111	25	145	Low ratio
4019	1 : 1	4186 B	80	32	108	
4089	1 : 5	4288 B	9	4	21	
4089	1 : 5	4290 B	70	27	88	
4089	1 : 5	4291 B	87	38	127	
4089	1 : 5	4292 B	96	36	120	
4091	1 : 2	4312 B	20	50	61	Mother both wings blistered
4091	1 : 2	4313 B	33	55	70	Mother both wings blistered
4090	2 : 1	4315 B	44	77	91	Mother both wings blistered

A second set of crosses selected blistered females and their normal brothers from the same F_1 (table 88). This shows that the blistered females with their normal brothers tend again to produce the same ratios as prevail generally. There are contained in this series four broods from parents with a large excess of blistered (1 : 5) which behave like the others. But three broods bred from females with both wings blistered produced an offspring with a 1 : 2 ratio. In a general way, then, the blis-

tered females breed like their nonblistered sisters, though the type with both wings blistered seems to have a genetic basis.

Only one F_3 from blistered females was bred:
No. 4445 (from ♀ blist. 4292): 89 ♀ 17 ♀ blist 90 ♂

There were two F_3 bred from normal sisters (out of blistered grandmothers) (see table 89). The results are of the type found before for nonblistered or blistered

TABLE 89

No.	Parent's no.	♀	♀ blist	♂
4335 B	4135	87	8	98
4336 B	4135	85	32	103

mothers. In F_4 from the F_2 4335 with 1/11 blist. flies (from normal parents) were obtained:

No. 4513 65 ♀ 12 ♀ blist 59 ♂
No. 4537 42 ♀ 7 ♀ blist 5 ♂

i.e., again low ratios of blistered, apparently a successful selection.

A third group of selections from the same F_1 group was made with both parents blistered (see table 90). Again the same irregular results appeared and the number of blistered males was not increased. F_3 from these, again with both parents blistered, gave:

No. 4370 (from 4184) 95 ♀ 21 ♀ blist 119 ♂ No. 4442 (from 4269) 72 ♀ 20 ♀ blist 66 ♂

which is actually a lower ratio for blistered.

There is no need to go into the details of further generations. It turned out to be impossible to produce by selection either a line without blistered flies, or with only blistered females, or with males as well as females blistered, though all this was produced later after spontaneous changes had taken place in the stock. Only the low incidence of blisters seemed to yield to selection.

All this applies to work done with the stocks while they remained fairly constant. I have already mentioned that, more recently (1940), blistered flies disappeared from the stocks. As this happened in all the stocks, obviously some unknown feature (food?) must have made this type less viable so that the modifiers needed for blistering were counterselected. In this case, however, as opposed to the former experiments, selection was completely effective, as may be illustrated by one example:

1st generation (pair matings):
a) 54 ♀ 5 ♀ bl
b) 62 ♀ 2 ♀ bl
c) 17 ♀
2d generation from a blistered female:
91 ♀ 17 ♀ bl
3d generation from a blistered female:
74 ♀ 15 ♀ bl 2 ♂ bl among 90
4th generation:
a) from ♀ and ♂ bl:
49 ♀ 21 ♀ bl 76 ♂ 1 ♂ bl
b) from ♀ bl:
76 ♀ 46 ♀ bl 132 ♂ 3 ♂ bl.

Stock remained constant in following generations. But when checked a year later, this selected stock had again returned to little blistering.

We return to the selection experiments in the original stock, performed before 1936. As the sex ratio is about normal, both in the stock and in the selections, the absence of blistering in the males cannot be due to lethality. But we saw that the number of rare blistered males is the same as that of rare double-blistered females;

TABLE 90

P. no.	F_1 ratio	No. F_2	♀	♀ blist	♂	♂ blist
4020	1 : 1	4183 B	31	13	43	..
4020	1 : 1	4184 B	36	14	45	2
4028	1 : 1	4192 B	49	17	68	..
4060	3 : 1	4269 B	87	28	100	1
4075	3 : 1	4296 B	16	37	47	..

further, that the males are always behind the females in plexation, and that in the just-reported broods with numerous blistered males their number is behind that of the females. We conclude, therefore, that whatever causes the blistering acts in the males only at a higher level than in the females. This conclusion will be borne out in crosses producing blisters by other means, as was shown to be true in the Px compounds.

In the following enumeration we tabulate the entire set of data, which include additional broods not mentioned in this chapter. Only the type of the parent of a brood is given, irrespective of the ancestors (blistered or not). All combinations were made within the original plexus blistered stock, i.e., before 1936.

1) 57 broods, both parents not blistered:
3152 ♀ 1181 ♀ blist. 72 ♀ both wings blist. 4223 ♂ 42 blist.
Sex ratio 103 : 1. Percentage ♀ blistered among ♀ = 28.4 per cent, ♂ bl = 1 per cent.
The ratio of n not blistered ♀ : 1 blistered ♀ is found in X broods:

n =	0–0.5	0.5–1.5	1.5–2.5	2.5–3.5	3.5–4.5	4.5–5.5	5.5–6.5	6.5–7.5 and above
X =	1	13	9	9	3	7	4	8

2) 26 broods, both parents blistered:
1402 ♀ 556 ♀ blist. 20 ♀ both wings blist. 1778 ♂ 34 ♂ blist.
Sex ratio 1.08 : 1. Percentage ♀ blistered among ♀ = 29.2 per cent, ♂ bl. almost 2 per cent.
The ratio of n not blistered ♀ : 1 blistered ♀ is found in X broods:

n =	0–0.5	0.5–1.5	1.5–2.5	2.5–3.5	3.5–4.5	4.5–5.5	5.5–6.5	6.5–7.5 and above
X =	2	2	5	5	5	1	1	1

3) 4 broods, ♀ not blistered × ♂ blistered:
337 ♀ 139 ♀ blist. 4 ♀ both wings blist.
489 ♂ 6 ♂ blist.
Sex ratio 0.97 : 1. Percentage ♀ blistered among ♀ = 30 per cent ♂ = 1.2 per cent.
Ratios ♀ : ♀ blist. : 1.2 2.4 3.9 4.4 : 1

4) 47 broods, ♀ blistered ♂ not blistered:
2703 ♀ 1191 ♀ blist. 48 ♀ both wings blist. 3577 ♂ 50 ♂ blist.
Sex ratio 1.09 : 1. Percentage ♀ blistered = 36 per cent ♂ = 1.4 per cent.
The ratios of n not blistered : 1 blistered ♀ are found in X broods:

n =	0–0.5	0.5–1.5	1.5–2.5	2.5–3.5	3.5–4.5	4.5–5.5	5.5–6.5	6.5–7.5 and above
X =	2	13	11	7	4	1	3	3 2

Conclusions: The foregoing data suggest that blistering in the stock, together with the high grade of plexation, is based upon a homozygous genetic condition, namely,

homozygosity of px bs with a series of special features: (1) There is a sex-limited expressivity, males tending to lower plexation and a threshold for appearance of blistering which is only rarely (1 per cent) surpassed. (But a higher allele of bs^p has arisen repeatedly, which affected males almost as much as females.) (2) The

TABLE 91

F_2 AND RF_2 OF px bl × N

Cross	No. of broods	Not px		px		blist	
		♀	♂	♀	♂	♀	♂
1. (px bl blist × N)²	12	740	536	279	178	25	1
2. (px bl × N)²	24	1446	1150	503	373	13	..
3. (N × px bl)²	16	1184	913	429	270	8	7
4. (N × px bl blist)²	7	572	469	149	114	..	..
5. ($\underline{Y}$ × px bl)²	13	560	399	157	108	..	7
6. (px bl blist × N) × recipr.	51	4940	4054	919	546	1	..
7. (N × px bl) × recipr.	7	501	372	174	127	24	1
8. (px bl × N) × recipr.	11	810	721	262	198	2	..
Total	141	10753	8614	2872	1914	63	16

percentage of blistering in females shows also an incomplete expressivity, as all-blistered lines cannot be selected. This may be a threshold condition, but it may also be due to special balances of modifiers. A threshold for penetrance is more probable. (3) There are modifiers present for lowering the expressivity of blistering which are subject to experimental as well as to chance selection under some environmental

TABLE 92

DISTRIBUTION OF BROODS WITH BLISTERED FLIES AMONG THE EIGHT TYPES OF CROSSES FROM TABLE 91

F_2 broods without blisters	120
F_2 broods with blisters	29
of these latter in group 1	8 out of 14
2	7 out of 25
3	2 out of 19
4	2 out of 9
5	3 out of 13. Only ♂
6	1 out of 51. (Only one ♀)
7	5 out of 7. Mostly ♀
8	1 out of 11. Only ♀

conditions, and for which return selection is possible. But they never could be selected beyond an average expressivity of 3 not blistered : 2 blistered.

Blistering after outcrossing.—If blistering were only the fluctuating effect of the homozygous px bl second chromosomes, F_2 from crosses ought not to differ from px bl within the plexus flies containing both px bl second chromosomes except for crossing over of eventual second-chromosome modifiers. Actually this is not the case. Out of about 150 such F_2 crosses about four-fifths of the broods with thousands of flies did not contain a single blistered fly though the mother or father came from

a px bl line with high incidence of blisters or were themselves blistered. Tables 97–93 contain the details. Table 91 lists the types of crosses in eight different categories. (px bl × N)^2 means F_2 from px bl females with a male of some standard stock not containing dominants, deficiencies, known rearrangements, or px or bs or ba alleles; px bl blist means that the P ♀ or ♂ was blistered. The mark × recipr. means the double reciprocal cross, which introduces different X chromosomes into

TABLE 93

SEGREGATION IN CROSSES PRODUCING BLISTERED FLIES, AS SUMMARIZED IN TABLE 92

No.	Cross type	not px		px		px blist		ratio not px : 1 px		
		♀	♂	♀	♂	♀	♂	♀	♂	
73	1	42	27	33	17	1	..	1.4	2.0	
74	1	68	50	22	14	1	..	3.1	3.6	
76	3	40	47	35	25	3	3	1.1	1.4	2♀ px bl w (w × px bl)^2
78	3	76	73	35	15	6	4	1.8	3.8	1♀ px bl w
84	1	79	61	44	30	4	..	1.6	2.0	(px bl × w)^2
85	1	85	12	29	9	7	..	2.4	3.2	(px bl × w)^2
86	1	73	63	13	19	8	..	3.5	3.3	(px bl × w)^2
396	1	50	41	24	18	1	1	2.4	2.3	
406	2	47	53	23	18	2	..	2.1	3.1	
416	7	58	40	20	7	4	1	3.1	6.1	
417	7	72	65	25	26	5	..	3.1	2.5	
418	7	71	50	28	19	3	..	2.7	2.6	
448	8	62	62	27	21	2	..	2.4	3.0	
452	7	53	50	22	10	4	..	2.6	5.0	
453	7	51	54	28	19	8	..	2.1	2.8	
463	4	47	32	17	..	2	1	2.5	32	Count not reliable
473	2	76	54	20	5	1	..	4.	11	
475	2	44	30	19	5	1	..	2.2	6	
476	2	41	25	24	19	3	..	1.8	1.3	
482	2	61	55	14	13	1	..	4.4	4.2	
483	2	61	48	24	13	4	..	2.7	3.7	
485	1	75	52	23	3	2	..	2	17.3	
487	1	71	48	25	10	1	..	2.7	4.8	
254	5	38	26	11	9	..	3	3.5	2.2	
261	5	31	19	11	4	..	2	2.8	3.1	
290	5	52	44	18	11	..	2	2.9	3.4	
456	2	57	44	26	16	1	..	2.1	2.8	

Further, one type 4 not properly classified.

the F_2 females as compared with the simple F_2. The broods with and without blistered flies are listed in table 92. (In tables 92 ff. a few broods have been added not contained in table 91 because only the px flies had been counted.) There is only one group, 6, almost completely without blistered flies, that is, one brood out of 51 with one blistered female. In three groups, 1, 2, 7, many broods contain blistered flies; in the groups 3, 4, 8 only few broods contain blistered flies, and group 5 contains only blistered males. The groups 1, 2, 7 contain crosses which all produce in F_2 one-half females with both X chromosomes from px bl stock. In the groups 3, 4, 6, 8 such a combination is not possible. In group 5, the y cross, only males receive an X chromosome from px bl. This grouping suggests that the presence of the two X

chromosomes (or one hemizygous X) from px bl stock allows for or increases the production of blistered flies, whereas the heterozygous condition of the px bl X only rarely allows the appearance of blistered flies. In some way, then, the X chromosome is involved.

Tables 91 and 92 demonstrate that, in the groups of F_2 which permit a recombination of two X chromosomes from px bl (1, 2, 7), 20 out of 46 broods produce blistered flies. In the groups which do not permit F_2 combinations of two X chromosomes from px bl, namely, 3, 4, 5, 6, 8, only 6 out of 103 broods contained blistered females, altogether about a dozen individuals among thousands of flies. Among these are the double-yellow crosses (5) without px bl X chromosomes (♀) and without blistered females, and the huge series 6 with 51 broods and only one blistered fly. This suggests that typically no blistered females are found in the absence of the two X chromosomes from px bl stock, but that a few exceptions exist which have to be accounted for. They may be modifications or results of a rare crossing over.

The details of the F_2 broods containing blistered flies are found in table 93. We begin with group 7, where 5 out of 7 broods contained blistered flies. All 5 belonged to one set of experiments (see below, table 94) in which all combinations of type 7 threw blistered flies. Type 7 is the double reciprocal cross $(N \times px\ bl) \times (px\ bl \times N)$. It differs from all other combinations leading to two X from px bl in F_2 in so far as the F_1 mother received her X from the px bl father. We might therefore assume that the enhancer for blistering is always (or almost always) present in the px bl males. We remember from the analysis of pointed that the male X chromosome is different from the female ones, by always containing a transposition because one class of crossovers between the points involved is lethal. The ratio of females px : px blist in the F_2 crosses, type 7, is 123 : 24. If we assume on the basis of the former discussion that only females with both X from px bl are blistered, the ratio of blistered among these females is $\frac{147}{2}$ — 24 : 24, i.e., 50 : 24 or 2 : 1, i.e., the ratio frequently found in the px bl line (see below).

In types 1 and 2 both X chromosomes from px bl recombined in F_2 are derived from the original mother. If a homozygous enhancer is needed for blistering, the situation does not differ from that in class 7. The normal broods which appear, more than one-half of the broods, suggest another complication, which will be discussed later. This group of data is, then, in favor of the need for homozygosity of the px bl X chromosome for the enhancing of blistering. The ratio of blistered flies in groups 1 and 2, calculated as before, is $\frac{401}{2}$ — 38 : 38 = 162 : 38 = about 4 : 1. This is a lower ratio than before. Looking at the data, it seems to be the average of two different groups: one with a high percentage, namely, 34 : 22, and another with a low percentage, namely, 129 : 16, both found in px bl stock, and indicating some other modifying influence, not yet accounted for.

We turn now to the large group of F_2 which does not contain two px bl X chromosomes, where we found 97 out of 103 broods without blistered flies. Of the six broods with blistered flies, one belongs to type 8, with 2 blistered females among 29 px females, (i.e., in the group, 2 among 264); one belongs to type 6, with 1 blistered female (i.e., 1 among 920); and two belong to type 4. One of the latter is not included in table 93 because the flies were checked only for highest-grade px. In one

(yvf × px bl blist)², no. 463, there was 1 female each in the + and y (crossover) class blistered. In the other (464) there were 3 ♀ +, 1 y, and 1 vf blistered, which among 68 ♀ (+ and px) is a rather high percentage. No interpretation for these exceptions

TABLE 94

SERIES OF F_2 CROSSES MADE SIMULTANEOUSLY BETWEEN px bl AND y v f; RELATED GRANDPARENTS AND PARENTS

No.	Type	F_1 no.	not px		px		not y v f blist	
			♀	♂	♀	♂	♀	♂
396	1	273	57	41	23	18	1	..
406	2	275	49	53	21	18	2	..
407	2	276	69	70	32	30	..	..
458	2	322	39	36	20	14	..	..
461	2	323	73	47	19	21	..	..
472	2	351	89	57	30	11	..	..
473	2	351	77	54	19	5	1	..
474	2	351	51	47	19	17	..	..
475	2	346	44	30	19	15	1	..
476	2	346	44	25	21	19	3	..
477	2	346	53	26	15	12	..	..
478	2	346	35	35	15	10	..	..
479	2	346	41	40	9	12	..	..
480	2	346	39	31	11	11	..	..
481	2	346	55	51	16	13	..	..
482	2	337	62	55	13	13	1	..
483	2	337	65	48	20	13	4	..
499	2	367	45	14	12	4	..	..
500	2	367	47	56	42	21	..	..
502	2	367	59	49	29	13	..	..
390	4	267	61	55	24	29	..	..
391	4	267	47	50	21	21	..	..
494	3	360	51	68	20	20	..	..
495	3	360	96	75	27	24	..	..
496	3	360	55	43	12	13	..	..
497	3	360	86	77	37	13	..	..
414	6	272 × 267	44	22	13	5	..	..
433	6	274 × 269	61	16	16	17	..	..
416	7	270 × 275	62	41	16	6	4	1
417	7	270 × 275	77	65	20	26	5	..
418	7	270 × 275	74	50	25	19	3	..
452	7	309 × 305	57	50	18	10	4	..
453	7	309 × 305	59	54	20	19	8	..
444	8	295 × 294	62	73	20	17	..	..
445	8	295 × 294	67	59	18	18	..	..
448	8	295 × 294	64	62	25	21	2	..
492	8	367 × 361	97	69	26	17	..	..
493	8	363 × 361	91	64	25	27	..	..

can be offered aside from the always available statement that some unknown modifier was introduced into the cross. (Also a rare dominance effect of the X-chromosome condition might be invoked, or a multiple crossover.) The two remaining exceptions, nos. 76 and 78, table 93, belonging to crossing type 3, are remarkable.

Here a relatively high percentage of blistering occurred; further blistered flies were found in + and w ♀, i.e., heterozygous for the px bl X chromosome and those without it, but for undetectable crossovers—cross: $(m \times px\ bl)^2$; finally, there were about as many blistered males as females, a very unusual feature (both F_2 were bred from brothers and sisters). We shall soon describe a similar case in which another bs allele (bs^{pp}) was responsible for the result. As no further analysis was made at the time, we can only register the exceptional case, though it is almost certain that it was another instance of crosses involving bs^{pp} (see below).

In order to demonstrate the regularities which have been observed thus far, we present in table 94 a series of 38 F_2, all made in different directions (see column "type") between the same px bl line with high incidence of blisters and a y v f stock. All crosses were made within three days and kept side by side. Frequently a series of F_2 were bred from brothers and sisters (see column F_1). We see that among 38 broods 25 had no blistered flies; among 19 broods of type 2, 6 had blistered flies; the only brood in type 1, the same; and all 5 broods of type 7 contained blistered flies. These are the three types with both px bl X chromosomes present in half the F_2 females. Groups 3 and 6 had no blistered flies in 6 cases; and groups 4 and 8 together had 1 case among 8 (to which the two exceptional cases 463 and 464 just discussed ought to be added). We note especially that the crosses in type 7, all of which gave a high percentage of blistered flies, were derived from 4 different F_1. The rules found for the whole series hold clearly for this strictly comparable series and are not chance products of environmental or genetic modification.

We have finally to report upon the behavior of F_3 derived from F_2 with and without blisters, bred, of course, from px flies. F_2 without blisters, independent of the type of the cross (except the y crosses), may produce all imaginable types in F_3. For example, 8 F_3 from F_2 type 3 without blisters produced 2 broods without blisters, a condition which remained in further generations; further, there were produced 4 broods containing a small percentage of blistered flies (about 5 per cent), and 2 broods with about one-half blistered flies, which latter continued breeding like ordinary px bl stock. Similar results were obtained from type 2 F_2. For example, from the F_2 type 2 tabulated in table 94, F_3 was bred without and with blistered flies. The former bred true to nonblistering, the latter produced the different types, among them also the typical px bl condition with $\pm$ ⅓ blistered flies. Example: F_3 from 482: (no. 558) 53 ♀ px 36 ♀ blist, 56 ♂ px 2 ♂ blist. Finally, marked third and fourth chromosomes recombine freely with blistering, so that the third and fourth chromosomes are hardly involved. It ought to be added here that neither svr^{poi} nor bran are present, as one might suspect in view of the fact that bran + poi = soft blistered. But in this case all ♀♀ and ♂♂ are blistered and, in the presence of px, are hardly viable (see above). In addition, no bran or poi ever segregated in these crosses.

We must now try to understand the facts and to relate them to the normal condition in the px bl stock. The following facts have to be brought into line.

1) In the original px bl stock percentages of 20–50 per cent blistered females and only 1 per cent males were constant.

2) Blistered and nonblistered ♀♀ and ♂♂ produced the same offspring.

3) Selection for absence or higher incidence of blisters was practically ineffective, though some result was obtained with low incidence of blisters.

4) The bs allele bs^p in px bl does not produce blisters, either alone or in combination with px, but considerably so in compound with a bs deficiency.

5) Sometimes there is present in px bl a higher allele bs^{pp} which in compound with bs^p produces blisters in both sexes in the presence of px/px. It seems always to be linked with a lethal.

TABLE 95

VARIATION OF THE F_1 PHENOTYPE IN DIFFERENT px bl CROSSES, NAMELY, + × px bl (TABLE 95), px bl × + (TABLE 96) AND $\underline{y}$ × px bl (TABLE 97)

No.	Cross	♀				♂			
		CV + EV	CV	EV	+	CV + EV	CV	EV	+
1	♀ + × ♂ px bl	23	6	20	..	..	..	30	11
2	♀ + × ♂ px bl	55	30	8	8	9	21	12	52
3	♀ + × ♂ px bl	44	20	9	10	1	5	13	54
4	♀ + × ♂ px bl	39	45	6	9	6	12	9	54
5	♀ + × ♂ px bl	28	55	6	25	3	9	13	87
6	♀ + × ♂ px bl	38	5	11	4	..	1	25	24
7	♀ + × ♂ px bl	10	7	..	1	..	2	1	4
8	♀ + × ♂ px bl	29	17	9	7	1	3	2	15
9	♀ + × ♂ px bl	45	9	7	8	..	6	8	44
10	♀ + × ♂ px bl	15	19	2	5	..	7	4	16
11	♀ + × ♂ px bl	20	27	7	27	1	3	5	81
12	♀ + × ♂ px bl	29	25	3	6	1	1	9	32
13	♀ + × ♂ px bl	26	20	5	5	1	4	11	27
14	♀ + × ♂ px bl	34	20	5	3	..	8	6	71
15	♀ + × ♂ px bl	17	23	2	6	..	4	4	52
16	♀ + × ♂ px bl	37	15	6	1	3	6	12	25
17	♀ + × ♂ px bl	37	25	3	2	8	7	4	40
18	♀ + × ♂ px bl	20	65	1	13	2	17	1	61
19	♀ + × ♂ px bl	23	53	14	36	4	14	12	82
20	♀ + × ♂ px bl	20	47	7	30	4	7	12	76
	Total	586	531	131	206	44	147	193	888

6) Outcrosses show that (in the absence of bs^{pp}) the condition of blistering found in px bl requires the presence of the original intact X chromosomes (in the presence of the original second chromosome).

7) The crosses with px bl ♂ suggest that the enhancer might be a transposition identical with or comparable to the one described for the X chromosome of pointed.

But this still cannot be the entire story (aside from modifiers). If the blistering is only produced by the combination of the original first and second chromosomes, all F_2 flies from broods which segregate this combination in one-half of the px flies ought to behave like the pure px bl stock except for crossing over. But actually half of the broods do not contain blistered flies, and it is possible to breed from such F_2 constantly normal as well as constantly blistered lines. It must therefore be assumed that in px bl a condition exists which is not necessarily present in extracted F_2 homozygous for both second and first chromosomes. As such a condition cannot be referred to enhancers in other chromosomes, the assumption is forced upon us that

some balanced condition exists within the px bl stock which prevents the formation of the types of broods without blisters, which, however, can be obtained after crossing.

We anticipate here that in the right end of the second chromosome of px bl two small deficiencies are found in the salivaries, both heterozygous. The first is probable always present (i.e., in half of the slides px bl × +), namely, a one-band deficiency (?) at the px locus (see discussion below); the second, a two-band deficiency

TABLE 96

No.	Cross	♀				♂			
		CV + EV	CV	EV	+	CV	CV + EV	EV	+
1	♀ px bl × ♂ +	42	25	11	7	7	1	1	27
2	♀ px bl × ♂ +	32	12	2	1	4	..	1	16
3	♀ px bl × ♂ +	20	37	2	8	12	2	2	30
4	♀ px bl × ♂ +	34	24	2	2	18	..	3	50
5	♀ px bl × ♂ +	21	50	1	2	14	..	1	28
6	♀ px bl × ♂ +	45	10	1	..	14	5	2	24
7	♀ px bl × ♂ +	22	44	2	6	18	..	2	23
8	♀ px bl × ♂ +	25	31	1	3	8	..	..	25
9	♀ px bl × ♂ +	30	9	4	4	12	1	4	34
10	♀ px bl × ♂ +	21	21	..	3	26	4	..	27
11	♀ px bl × ♂ +	30	17	6	1	18	3	2	30
12	♀ px bl × ♂ +	63	23	2	1	36	11	5	32
13	♀ px bl × ♂ +	15	15	1	2	4	3	1	10
14	♀ px bl × ♂ +	31	46	..	2	14	1	..	24
15	♀ px bl × ♂ +	23	36	9	12	8	4	1	39
16	♀ px bl × ♂ +	25	6	5	2	14	4	2	21
17	♀ px bl × ♂ +	22	6	3	1	3	4	4	18
18	♀ px bl × ♂ +	..	4	1	..	7	..	1	8
19	♀ px bl × ♂ +	13	32	2	20	6	1	..	34
20	♀ px bl × ♂ +	25	38	2	5	20	2	3	41
	Total	539	486	57	82	264	46	35	541

to the right of bs ba, is less frequent. Together they could provide a balance for the second chromosome. We know already that px bs^p/px bs^p has no blisters in the presence of the proper XX. If we call the px deficiency px^D, the combination $px^D bs^p$/px bs^p is also without blisters or with only rare blistered flies in the absence of the proper X chromosomes. But in the presence of these X chromosomes we find the standard incidence of blisters. Thus a cross $px^D bs^p$/px bs^p × + gives two types of F_1, namely, $px^D bs^p$/+ and px bs^p/+. F_2 from the latter will not produce blistered flies even with the original two X chromosomes. This, then, would explain the actual results. A check could be derived from the ratios of segregating plexus. In the presence of $px^D bs^p$/+ F_2 could be obtained from both parents of this constitution, which means that only a few px flies (from crossover px–bs) could appear if px^D/px^D is lethal. The data do not answer this question.

Another test was tried, namely, a careful phenotypical check of F_1 and the breeding of F_2 from different types. Actually, F_1 seemed to indicate the presence of a

heterozygotic condition in the px bl parents. Twenty F_1 crosses each were made px bl × Oregon and reciprocal with the then constant px bl stock, throwing about 20–40 per cent blistered females. In addition, the cross y × px bl was made as a check for the X-chromosomal effect.

In tables 95–97 the results of these three groups of 20 F_1 each are tabulated. CV means individuals with branch at the cross vein, EV = extra vein in 5th cell (V), CV + EV = both, + = none. We notice that in both reciprocal crosses about ½ of the

TABLE 97

No.	Cross	♀				♂			
		CV + EV	CV	EV	+	CV + EV	CV	EV	+
1	♀y ♂ px bl	..	..	12	14	..	..	..	5
2	♀y ♂ px bl	..	..	14	37	..	..	..	51
3	♀y ♂ px bl	..	..	..	20	..	..	..	19
4	♀y ♂ px bl	..	..	8	20	..	..	..	21
5	♀y ♂ px bl	..	1	24	28	..	..	10	56
6	♀y ♂ px bl	..	..	19	20	..	..	8	29
7	♀y ♂ px bl	1	..	13	20	..	..	1	27
8	♀y ♂ px bl	..	..	13	19	..	..	2	47
9	♀y ♂ px bl	..	..	24	17	..	..	5	33
10	♀y ♂ px bl	..	..	18	13	..	..	9	39
11	♀y ♂ px bl	..	..	11	12	..	..	6	50
12	♀y ♂ px bl	..	..	14	29	..	..	..	54
13	♀y ♂ px bl	..	..	26	5	..	..	3	14
14	♀y ♂ px bl	..	..	23	32	..	..	6	51
15	♀y ♂ px bl	..	..	13	17	..	..	5	36
16	♀y ♂ px bl	..	..	20	19	..	..	7	35
17	♀y ♂ px bl	..	..	6	23	..	..	..	39
18	♀y ♂ px bl	..	..	14	21	..	..	2	98
19	♀y ♂ px bl	..	..	15	24	..	..	..	46
20	♀y ♂ px bl	..	..	15	21	..	..	1	45
	Total	1	1	302	412	..	..	65	746

♀ have the extra vein, whereas the majority possesses the branch of the cross vein. In most cases only a few + individuals are found, which might represent minus individuals of the CV class. But in a few cases large numbers of plus males seem to be significant. In the males, however, the plus individuals are in the majority, and only a minority of CV and EV are found. But we have to be prepared here, as always in these crosses, for a shift to the minus side in the males. Most conspicuous is, however, the difference in the y crosses. The second chromosome is heterozygous as in the others, but in the females the X from px bl are absent. In these females only two individuals with a branch of the cross vein were found, and in the males the CV class is completely absent. EV transgressing into + is known to be the heterozygous bs effect, with few + flies among the females and many among the males. CV is then supposed to be a heterozygous px effect. In the females there is certainly no segregation for the CV effect. In the males it looks as if such a segregation were visible in px bl × plus, but not clearly in the reciprocal cross. Thus if the mothers

were actually $px^{D}bs^{p}/px\ bs^{p}$ in F_1 ♀ $px^{D}/+$ and $px/+$ are not distinguishable, though possibly this is the case in males. But in the males there is apparent also a considerable shift toward normal in the absence of the px bl X chromosome. Most disconcerting are the perfectly regular results of the y crosses with practical absence of the CV classes. As the females do not have any X chromosome from px bl stock, one might think that this is responsible. But the males have such an X. We remember, however, that in pointed the male X differs from the female by always containing the transposition. Whether the same condition is involved here or whether y introduced a dominant modifier could not be decided.

Thus it was hoped that blistering and px segregation in F_2 from selected F_1 could furnish more information. Many F_2 were bred from the different types of F_1 and checked for all classes. Blistering occurred according to the rules discussed above, and px segregated in the different ratios to be discussed, but no clear correlation could be found. Thus it could not be decided whether the peculiarities of the inheritance of blistering were based upon px^{D}, or an independent dominant modifier, or the presence of another bs allele otherwise indistinguishable in its effects. The data to be reported below on the allele bs^{pp} make me favor the explanation by the px deficiency. It ought to be added that the localization of the X-chromosome enhancer for blistering did not succeed because among the few blistered F_2 flies in crosses with marked X only very few were found in crossover classes, as has already been noted.

A short general remark may be added regarding blistering apart from the blistering involving the bs and ba stock. Blisters have been described also in translocation and similar stocks, though I do not know of a special inquiry into their appearence. In practically all stocks an occasional fly with blisters is found as a not heritable condition, as it seems, and in temperature experiments blistered wings may be produced as a phenocopy. I noticed years ago that a wild stock from Lausanne, kept in my Berlin-Dahlem laboratory, regularly threw blistered flies. Twenty-four pair matings in three generations yielded 3300 ♀♂, 30 ♀ 3 ♂ blistered. Fifteen of the twenty-four broods contained 1–5 blistered flies. Among the offspring of blistered flies the same ratio appeared, namely, 950 ♀♂, 10 ♀ blistered. Other wild stocks bred side by side with the Lausanne stock hardly ever contained a blistered fly. There was certainly some genetic reason for the behavior of the Lausanne stock.

Blistering due to the allele bs^{pp}.—At the time when we were trying to analyze the complicated situation regarding the blistering in the px bl stock at the same time that the selection experiments were performed (see p. 423) an unexpected result was realized. From a pair of normal px bl flies of the usual type and from a typical line throwing 30–50 per cent blistered females, a brood was derived:

4059 58 ♀ px bl 6 ♀ blist 39 ♂

i.e., an excessively low percentage of blistered females for this line, and a low sex ratio.

From this, 2 broods from not blistered pairs were derived:

4222 13 ♀ 3 ♀ blist 13 ♂
4223 104 ♀ 19 ♀ blist 2 ♀ both wings blist 173 ♂

again a low percentage of blistered females, no blistered males. In the next generation 2 broods from normal females with brothers were bred:

4389 53 ♀ 12 ♀ blist 65 ♂ 2 ♂ blist
4390 1 ♀ 1 ♀ blist 5 ♂

From 4389 the following generation was bred:

a) From not blistered parents:
4539 38 ♀ 14 ♀ blist 44 ♂ 1 ♂ blist
b) From both parents blistered:
4540 35 ♀ 35 ♀ blist 3 ♀ both wings blist 73 ♂ 7 ♂ blist (3 ♂ hemithorax)

From both blistered parents, then, a high percentage of blistered females (50 per cent as opposed to 11 per cent in the first generation) was produced; further, a relatively high number of females with both wings blistered; and, finally, a very high percentage of blistered males (10 per cent; normally, 1.5 per cent). Again, a generation from both parents blistered was bred.

4677 23 ♀ 48 ♀ blist 70 ♂ 5 ♂ blist, i.e., more blistered females than not, and comparatively many blistered males

The next generation, 4856, had the same appearance but was not counted. But from this a stock was derived which contained almost exclusively blistered females and a high percentage of blistered males. Obviously the blistered male, father of 4540, had started the new condition, which bred true. It could be explained if there had arisen by mutation (or been rarely present in the stock) a higher allele of bs, namely, bs^{pp}, which in heterozygous condition increased the percentage of blistering in both sexes. At that time it was suspected that this aberrant behavior might be connected with a deficiency in the second chromosome. Therefore, the different types found in the stock (♀♂ not blistered and blistered) were crossed to b pr vg a sp (5 ple). No deficiency for these loci was present. Simultaneously, another line derived from px bl in which blistering had completely disappeared (px bl ll) was tested the same way and no deficiency was present. Now the two lines, px bl ll without blisters and low px, and px bl 4856 with extreme incidence of blisters (and plexation), were crossed. The result was:

5015 px bl 11 × 4856 ♂ not blistered:
7 ♀ px 31 ♀ px blist, about half both wings
38 ♂ px 4 ♂ px blist
5017 4856 ♀ blist × px bl ll
3 ♀ px 14 ♀ blist, mostly both wings
37 ♂ 2 ♂ blist

This cross, in both directions, then increased the blistered females to more than 80 per cent and simultaneously increased the amount of blistering (both wings). Two F_2 were bred, one from 5017 with normal flies (5236), one from 5015 with blistered flies (5240):

5236 = 5017² not blist:
12 ♀ 18 ♂ not blist
19 ♀ 8 ♂ blist
5240 = 5015² blist:
42 ♀ 109 ♂ not blist
47 ♀ 42 ♂ one wing blist
52 ♀ 28 ♂ both wings blist

In the larger brood, about ⅔ of the females and nearly ½ of the males were blistered, and about ½ of them on both wings. The new condition of high blistering was thus ± dominant in both sexes in the presence of homozygous px and of the bs allele bs^{p}, and the 2:1 ratio for females indicates lethality of the homozygote.

The 4856 stock was now tested in numerous crosses with the loci at the end of the second chromosome (px, bs, ba, a, sp, ll). Not a single case of deficiency was found, the only distinction from typical F_1 being that among thousands of flies 3 ♀ and 2 ♂ were blistered (i.e., a little dominance in the heterozygote). It ought to be mentioned that tests for the presence of pointed or bran were negative.

The next test was to find whether, as in ordinary blistering, the X chromosome was involved by combining the new condition with marked X chromosomes. It turned out that this blistering combined freely with foreign X chromosomes and

TABLE 98

TWELVE BACKCROSSES OF F_1 plexus blistered STOCK × white OR vermilion (6 EACH), WITH plexus blistered white (OR vermilion)

(Formulae in text. The first six are the white, the others the vermilion crosses.)

No.	+		w (v)		px		px w (v)		px bl		px bl w (v)		+ bl web		(v) w bl web	
	♀	♂	♀	♂	♀	♂	♀	♂	♀	♂	♀	♂	♀	♂	♀	♂
8369 B.....	21	21	10	25	2	20	3	19	12	3	5	4	..	2	..	..
8370 B.....	12	40	8	41	3	23	2	33	3	11	12	9	..	..	..	..
8371 B.....	17	22	15	23	5	14	5	14	8	7	12	4	1	..	..	..
8372 B.....	24	30	16	24	7	19	7	20	18	6	8	5	..	..	..	..
8374 B.....	18	40	9	34	3	27	..	24	10	23	12	8	..	..	..	..
8375 B.....	14	27	18	13	6	19	10	21	2	1	2	..	..	..	..	..
8377 B.....	22	28	13	26	6	16	7	20	24	2	13	6	..	..	..	..
8378 B.....	43	37	56	20	29	34	29	34	11	..	23	1	..	..	..	..
8379 B.....	16	25	27	12	11	22	3	15	17	7	8	7	..	..	1	..
8380 B.....	26	17	16	19	11	15	4	14	10	2	11	5	..	..	1	2
8381 B.....	21	24	19	20	4	23	7	11	14	3	15	5	..	..	3	3
8383 B.....	25	21	20	13	6	16	6	14	14	4	14	9	..	..	..	2
Total w.....	106	180	76	160	26	122	27	131	53	51	51	30	1	2	..	..
Total v.....	153	152	151	120	67	126	56	108	90	18	84	33	..	..	5	7

was completely (or almost) autosomal in origin. This permitted a test of the blistering effect in homozygous and heterozygous condition. Blistered females from the blistered stock were crossed with white (w) males and the F_1 females backcrossed to formerly extracted male px bl, w and blistered. If the blistered stock was homozygous bs^{pp}, the cross was:

1) px bs^{pp}/+, w/+ × px zs^{pp}/px bs^{pp}, w. The expectation is ½ like stock (with or without w), ½ w or +. This means that almost all px females and fewer males are blistered. If the blistered stock could be homo- or heterozygous bs^{pp} (compound with bs^{p}), the crosses might have been (omitting the w marker, segregating as before):

2) px bs^{pp}/+ × px bs^{pp}/px bs^{p} = among px flies in one half all ♀, in the other half many ♀ blist, i.e., about ⅔ blist; or

3) px bs^{p}/+ × px bs^{pp}/px bs^{pp} = among px flies half are not blist, of the other half only a part, i.e., about + ⅙ blist; or

4) px bs^{p}/+ × px bs^{pp}/px bs^{pp} = among px flies about ⅓–½ blist.

Table 98 contains the results of twelve such crosses, the first six of which were made with white, the other six with vermilion. The general segregation is the

expected one, i.e., ¼ +, ¼ w (v), ¼ px, ¼ px w (v). Looking over the px class, we find (aside from the expected different expressivity of blistering in the two sexes, in the females, on the average, a ratio of less than 2 ♀ blist : 1 not. The individual crosses fall clearly into four groups:

1) No. 8374, with almost all ♀ and ½ of the px ♂ blistered, may represent the first type of cross just enumerated as possibilities 1–4.

2) No. 8375, with only a few ♀ and ♂ blistered, may represent the cross type 3.

3) No. 8378, with about ⅓ ♀ and few ♂ blistered, may represent type 4.

4) All others, with about ⅔ ♀ and many ♂ blistered, may represent type 2.

In the crosses of type 4 also, bs^{pp}/bs^{pp} px can be produced by crossing over, thus showing the phenotype of bs^{pp} alone if viable. Actually, 6 ♀ 9 ♂ of this crossover type (c.o. px–bs) are found (the reciprocal class being px and not distinguishable, though they might eventually have been distinguished by low plexation). The phentoype is exactly as described before for bs^{pp}, namely, a broad web with a blister on top. The percentage of crossing over is rather low. Attention is directed to the strange sex ratios observed in these crosses. They will be discussed below.

In this case the pedigree makes it rather sure that the bs^{pp} allele had arisen by mutation from px bs^{p} in one individual. In former data we saw this allele occasionally present in the stock. In mass culture it cannot hold its own against bs^{p}. This was shown in the selected stock just described, which contained bs^{pp} but was, as it seems, not yet completely homozygous since it returned to the condition with little blistering, i.e., without bs^{pp}, during an interim of 1½ years when it was not checked while my work was being transferred from Berlin to Berkeley and Dr. C. Stern kindly kept the stocks alive. Later, the same allele bs^{pp} was once more selected out of the stock by chance. The standard stock had changed to a low blistering. By selection of blistered flies it was returned in a few generations to its old condition, i.e., by selection of modifiers (see above, p. 423). Simultaneously, Mr. M. Kodani made a parallel selection in order to have a good line for salivary work. By chance he hit upon a bs^{pp} allele and selected a stock with most females and may males blistered, i.e., bs^{pp}. There is still another case in which it seems that bs^{pp} had arisen anew by mutation. In one of the px bl bottles which had bred true to type for many generations (about 5 years) a breaking up of the type occurred, as described on pages 485 ff., with the production of wild type, low px without bs, pointed (the allele poi^{s} and others), and here also bs^{pp} was found, from which a typical line was isolated which bred true for the described characteristics, and showed also a tendency to an increase of the number of hairs upon the anterior end of the thorax and duplication of the anterior scutellars.

In the presence of the higher allele bs^{pp}, blistering is caused, so it seems, exclusively by this allele. But in the stock in which this mutant originated we reported an enhancer for blistering in the X chromosome which may still be present in the px bl line with bs^{pp}. Crosses with marked X chromosomes made to test this point gave rather strange results, as table 99 shows, for males (females being almost all blistered). In both groups of crosses the crossover conditions and relations of blistering to the X chromosome were tested. The first group (♀ blist $4856 \times$ y cv v f)[2] produced heterozygous females for the X chromosome, the two types of males, and the crossover males. All may recombine with px and with blistering, as the case may be; the table contains only the males. We notice that blistered males appeared

in almost all classes but in different ratios. In normal males, i.e., without homozygous px chromosome and with the X from the blistered stock, only 1 among 98 was blistered. This is actually a crossover px bs^{pp}/bs^{pp} ♂ = web blistered. The X chromosome is not involved here. In px males there were 2 among 37, which is a lower percentage than in the stock. In y cv v f males about the same percentage is present (2 in 30), showing, as proved before, that the X chromosome from the blistered stock is not indispensable for blistering. But in the crossover classes the incidence of blistering is much higher than in the noncrossover classes:

Non-c.o. classes px : px blist 63 : 4 = ca. 16 : 1
C.o. classes px : px blist 70 : 13 = 5.4 : 1

There is one crossover class, namely, y cv v, in which px and px blist are about equal (6 : 5). This suggests that though the blistering is predominantly autosomal, something in the X chromosome is also involved and is located somewhere between v and f. This conclusion is brought out also by the group of reciprocal crosses, table 99. Here the ratios are:

Non-c.o. classes px : px blist 52 : 4 = 13 : 1
C.o. classes px : px blist 56 : 12 = 4.7 : 1
y cv v px : px blist 3 : 7

In the same crossover class containing only the right end of the X chromosome, more blistered males appeared than normal ones.[11] The crossover values are hardly informative in view of the large distances involved. They are, with the standard value in parentheses, y–cv = 16.6 (13.7), cv–v = 24.7 (19.3), v–f = 20.5 (23.7).

Thus it appears that the enhancer for blistering was still present in the X chromosome when bs^{pp} originated and that it was located at the right end between v and f. But it cannot be as simple as that, as the noncrossover class shows: the intact X chromosome from px^{bl} 4856 does not enhance blistering, and neither does the chromosome without the y-containing tip. It seems that it is the absence of the cv–v region of this X chromosome in the presence of a section between v and f which does the enhancing. We remember that in pointed a comparable relation was found, namely, a transposition into the wy region from the left end which could produce by crossing over male lethal classes. In the present case, however, no male lethal class is present and therefore the transposition is ruled out. It may safely be assumed that the sex-linked condition enhancing blistering which had been found in the original stock but could not be localized on account of the paucity of the blistered crossover flies was the same as recorded here, and that one of the reasons for the low incidence of blistering in F_2 was the complicated setup of the enhancer, which the present data show but do not explain.

This sends us back to the crosses reported in table 98, i.e., (px bl bs^{pp} stock × white) × px bl ditto and w, and the same with vermilion. In this case, unique sex ratios appeared, never observed in other crosses with the px bl stock, and therefore characteristic for a condition present at the moment that the bs^{pp} allele had arisen. In all the crosses in which the paternal X chromosome contained the left end of the original X with the right end replaced (marked by v), the sex ratios are normal, once with a great preponderance of females (see table 100, where the blistered flies have not been separated from px). But in all the crosses in which the right end of

[11] Both y cv v groups added, i.e., 9 : 12, are statistically significant at and above a 3 : 1 ratio.

the paternal X chromosome was present with the left replaced by the chromosome marked with w, very abnormal ratios in favor of males are always present, in one case actually 1 ♀ : 4 ♂. In the two cases of the extreme ratios (1 : 3 or 4), all classes,

TABLE 99

Class	(X ple × px bl)² No. 7354–66 B	(px bl × X ple)² 7353–7447 B	Total	px : px bl
+	97 (+ 1 blist)	122	219	.....
+ px	35	32	67	33.5 : 1
+ px bl	2	..	2	.....
y cv v f	71	78	149	.....
y cv v f px	28	20	48	8 : 1
y cv v f px bl	2	4	6	.....
y	39	22	61	.....
y px	10	6	16	16 : 1
y px bl	1	..	1	.....
cv v f	13	19	32	.....
cv v f px	7	11	18	9 : 1
cv v f px bl	..	2	2	.....
y cv	42	37	79	.....
y cv px	10	8	18	6 : 1
y cv px bl	2	1	3	.....
v f	42	41	83	.....
v f px	15	14	29	14.5 : 1
v f px bl	2	..	2	.....
y cv v	22	27	49	.....
y cv v px	6	3	9	0.82 : 1
y cv v px bl	4	7	11	.....
f	19	36	55	.....
f px	12	7	19	6.3 : 1
f px bl	2	1	3	.....
y f	9	7	16	.....
y f px	2	2	4	.....
cv v	8	2	10	.....
cv v px	1	2	3	3 : 1
cv v px bl	1	..	1	.....
y v	..	1	1	.....
cv f	..	1	1	.....
y cv f	8	5	13	.....
y cv f px	2	3	5	5 : 1
y cv f px bl	..	1	1	.....
v	5	9	14	.....
v px	3	..	3	.....
y v f	..	2	2	.....
y v f px	2	..	2	.....
cv	1	2	3	.....
cv px	1	..	1	.....

+, w, px, and px w, show the low ratio. In the cases of less extreme ratios one or more classes seem to show a 1 : 2 ratio, others being normal, or some show a 1 : 2, others a 1 : 3 or normal ratio without any visible rule except in one case (no. 1), where both classes with w have the low ratio. Undoubtedly, the relation of right half to left half of the X chromosome is responsible and this points again to a trans-

position, which, however, cannot be the left–right transposition found in poi, which would produce male lethal classes with the left end without the right end of X. But it is very difficult to visualize how such a transposition could produce female-lethal classes in different combinations with autosomes. There is another possibility, which, however, accounts only for the females of the px classes. The salivary glands frequently show a two-band deficiency to the right of bs ba and sometimes an insertion near the tip of X which might be the same bands. Thus, flies with that insertion might be viable with the homozygous deficiency and not without. Actually, the crossover flies are in favor of this explanation. In the crosses involving an X

TABLE 100

(Table 98 rearranged)

Group	px		px w(v)		+		w(v)			Sex ratio
	♀	♂	♀	♂	♀	♂	♀	♂		
w group										
1	12	23	8	23	21	21	10	25	2 ♂ + bl web.....	51 : 94 = 1 : 1.8
2	6	34	14	42	12	40	8	41	.....	40 : 157 = 1 : 4
3	13	21	17	18	17	22	15	23	1 ♀ + bl web.....	63 : 84 = 1 : 1.3
4	25	25	15	25	24	30	16	24	.....	80 : 104 = 1 : 1.3
5	13	50	12	32	18	40	9	34	.....	52 : 159 = 1 : 3
6	8	20	12	21	14	27	18	13	.....	52 : 81 = 1 : 1.6
v group										
1	30	18	20	26	22	28	13	26	.....	85 : 98 = 1 : 1.2
2	40	34	52	35	43	37	56	20	.....	191 : 126 = 1.5 : 1
3	28	29	11	22	16	25	27	12	1 ♀ v bl web.....	83 : 88 = 1 : 1.1
4	21	17	15	19	26	17	16	19	1 ♀ 2 ♂ v bl web.....	79 : 74 = 1.1 : 1
5	18	26	22	16	21	24	19	20	3 ♀ 3 ♂ v bl web.....	83 : 86 = 1 : 1
6	20	20	20	23	25	21	20	13	2 ♂ v bl web.....	85 : 79 = 1.1 : 1

chromosome in which the tip marked by w has been replaced by crossing over, only not w ♀ and ♂ crossovers are found, i.e., flies px bs^{pp} Df/bs^{pp}, X from stock. In the crosses with X chromosomes marked by v, i.e., the left end derived from px bl present, it is the v class which contains the crossovers, i.e., px bs^{pp} Df/bs^{pp}, X left end from stock right end from v. But the insertion near fa was only found in poi, not in px bl. It is possible that it was exceptionally present here. But it is of no use to attempt any of these explanations in detail, since further analysis was prevented by the already mentioned circumstances. The data have been discussed in detail in order to show that we must reckon with the presence of many more abnormal conditions of the rearrangement type than can actually be localized.

f. THE PHENOTYPES WITHIN THE px bl STOCK

The foregoing data have shown the presence of px and bs^{p} in the px bl stock; further, the occasional presence of bs^{pp}, and also an enhancing condition in the X chromosome which increases blistering as well as plexation. As there certainly is environmental action also, it must be difficult by mere inspection to isolate the genotypes underlying the different degrees of plexation found in the stock. We have described above how some results could be accomplished by crosses with the Plexates which,

in some cases, permitted detection of bs^{pp} in the stock. We report here upon some experiments in which an attempt was made to check upon eventual different alleles of plexus as well as of bs and the enhancers. For our test, similar phenotypes from inbred px bl were crossed with a standard inbred px line (a px sp). The a px sp stock was rather homogeneous in phenotype. There was present more or less of a posterior branch of the posterior cross vein (CV), more or less of a vein (EA) in the fifth cell, a small antler attached to the second vein, and a long extra vein in the marginal cell. Only the extremest plus individuals showed a beginning of parallel and periclinal veins. Sometimes the CV appeared to be increased into a little net formation. Seven F_1 were studied in detail (2636–42). Two showed a plexus type not distinguishable from that of the a px sp stock. In two others approximately half the flies were a px sp-like (with respect to plexation). The other half showed a higher grade of plexus with web formation near the cross vein and in II; some individuals had minute blisters (like pearls) above the web in V. One showed in all individuals an intermediate condition between the two types just described. Two more contained half of the low types and half (approximately) of the medium types.

These F_1 types were backcrossed again to a px sp (2757–69). Five crosses from highest-grade F_1 plexus mothers were made, three of which yielded one-half a px sp type plexation and one-half the strong maternal type. The latter was present in px and a px sp flies equally, which indicates that it was not based upon a higher allele of px in the px bl stock, but upon a modifier in another chromosome or far away toward the left end of the second chromosome. In one more cross the high maternal type was absent, and in another it was very rare. Six backcrosses were made with the ordinary low type of F_1. Four of these yielded only low maternal type, but two gave the same segregation in low and high as the foregoing group (probably owing to transgressing variability in F_1). A few F_2 crosses agree in part with these results. In one case the extracted individuals with two px bl second chromosomes could not be distinguished from the heterozygotes. One F_2 from low F_1 reconstituted a low px bl type in one-fourth of the F_2 flies, namely, generally low plexation but with parallel and periclinal veins. F_2 from the high F_1, however, gave one-fourth high plexation, including large webs and some blistered females. In this latter case either a high allele of px or a higher allele of bs or an enhancer within the second chromosome might have been responsible.

Therefore the same problem was studied by classifying F_2 plexus individuals from different crosses with the px bl line, the other parent containing neither px nor dominant markers nor inversions (which latter can act as intensifiers). We have stated earlier that, as a rule, the px bl type is not recovered or only rarely recovered in F_2. In the majority of cases the higher types of plexus formation with parallel and periclinal veins and web are absent in F_2. In order to have a simple classification, we call the px type as found in the different standard px which we used (description, p. 405) a low plexus; if much plexus formation in the marginal and first cells is combined with a complete periclinal vein but lacks a parallel vein, we speak of medium grade; the addition of more or less of the parallel vein with much web formation is a high grade; and extreme grade, finally, increases the web formation, and has nets at all points of extravenation. There are, of course, all kinds of individual variations, hardly any two individuals being alike. Table 101 gives the results for many F_2 in these terms, adding, where noted, the condition of the P indi-

viduals from px bl. (I = low grade; IV = extreme grade.) As there is much transgression, the actual numbers of the classes are not very significant. The tedious classification has been made for over 90 F_2 broods by the same recorder (the senior author). In the table certain groups have been lumped together to avoid lengthy details, and only 78 strictly comparable F_2 have been included.

The most conspicuous fact, one which at once becomes evident from the table, is that the enhancer which produces the highest grade of plexus formation in the presence of homozygous px (and the bs allele) is located in the X chromosome. Whereas in all combinations F_2 females and males are more or less alike, with the males, on an average, in lower grades than the females, the F_2 with $\underline{y}$ grandmothers

TABLE 101

Cross or type of px bl grandparent	not px		px ♀ class				px ♂ class				No. of F_2
	♀	♂	I	II	III	IV	I	II	III	IV	
♀ IV blist. Group a	432	312	12	118	2	..	35	54	..	..	8
♀ IV blist. Group b	529	335	..	96	64	..	14	52	17	..	11
♀ IV blist. Group c	821	603	..	142	137	29	16	160	9	2	13
($\underline{y}$ × px bl ♂ III)²	614	426	19	148	..	..	..	96	18	7	14
♀ IV	169	127	..	26	36	3	21	4	26	..	3
♀ I	153	173	59	...	..	..	53	..	..	..	2
♀ III	506	451	..	112	55	4	8	122	15	..	7
♀♂ IV blist (double reciprocal cross)	109	105	..	22	5	..	5	8	1	..	2
♂ IV blist	108	103	..	35	..	3	3	46	..	1	2
♂ ? (II, III, IV) a	746	535	..	180	61	..	..	145	..	..	10
♂ ? (II, III, IV) b	420	323	..	58	83	24	..	56	53	1	6
Total	4607	3493	90	937	443	63	155	743	139	11	78

show the males in higher grades than the females. The X chromosome from px bl is therefore needed for the higher grades. If the grandmother was a higher-grade female (grade IV), the F_2 results may be distributed among three groups: a low one (*a*) with only low grades represented; an intermediate one (*b*) with the mean between II and III; and a high grade (*c*) with females of medium and high grades. The double reciprocal crosses which do not produce females with both px bl first chromosomes are of the lower type, as expected. Something in the X chromosome of the px bl, then, enhances the plexus formation.

It would certainly be difficult to disentangle the types completely. But it seems most probable that grades I and II are lacking the enhancer, as the $\underline{y}$ crosses and the crosses from grade I show. Classes III and IV, then, indicate the presence of the enhancer (probably with differences between homozygous and heterozygous females, which can hardly be distinguished), as the crosses involving grandparental males show, in which no homozygous female may exist (for the X chromosome). But it cannot be excluded that the crosses from type IV grandmothers indicate the presence of the enhancer as well as that of a higher px or bs allele. Much work was done in classifying px grades in crossover classes in crosses with marked chromosomes. The results were so irregular that this type of analysis was discontinued. To mention only one such result: in experiments with X-chromosome markers, both

females and males of class III were found in all crossover classes when only the loci y v f were involved, though among the males, at least, the majority of marked class III males appeared in classes containing yellow. In crosses involving more markers (X'), males III were found with y ec cv v, y ec cv, y ec cv ct v g, y ec v g f, and y ec; class IV males in the same crosses were found in y ec cv f and y ec cv ct.

g. OUTCROSSES AND RATIOS OF SEGREGATION

Returning to the problem of lethal classes which were found when bs^{pp} appeared, we have to study the segregation of the second chromosome marked by px, after outcrossing px bl to ordinary stocks. The ratio not px : px was calculated for 95 comparable F_2 crosses $(px\ bl \times N)^2$, separately for females and males. From these ratios

TABLE 102

F_2 RATIOS NOT px : px

No. of broods, ♀ and ♂	Ratio														
	-1.2	-1.4	-1.6	-1.8	-2.0	-2.2	-2.4	-2.6	-2.8	-3.0	-3.2	-3.4	-3.6	-3.8	-4.0
♀	1	1	1	3	3	8	7	5	9	5	6	6	6	10	7
♂	..	2	..	1	6	4	8	5	6	3	5	8	10	5	4

No. of broods, ♀ and ♂	Ratio													
	-4.2	-4.4	-4.6	-4.8	-5.0	-5.2	5.9	6.2	6.5	7.7	8	11	14	16
♀	4	5	5	1	2	3	2	..	1	..	..	..	..	..
♂	8	2	..	1	2	3	3	2	1	1	2	1	1	1

the frequency table 102 was derived. Practically all individual broods were good-sized; there were about 15,000 flies altogether. The individual ratios appeared so different that the presence of groups of ratios, 3 : 1 and others, were expected. Therefore the χ^2 values for all individual broods above 50 individuals were calculated for females and males and the homogeneity test was applied to larger groups. The result was: among the females of 93 broods, 82 fit a 3 : 1 ratio, i.e., P for $3:1 > 0.05$. The remaining 11 broods were tested for 1 : 1, 2 : 1, 4 : 1, 6 : 1, and 10 : 1 ratios. The χ^2 showed good fit for 1 : 1 in 4 broods, for 2 : 1 in 5 broods, for 4 : 1 in 4 broods, 6 : 1 in 4 broods, and 10 : 1 in one brood. The corresponding data for males were the following. There were 72 broods of sufficient size. Of these, 58 fit a 3 : 1 ratio. Of the 14 remaining broods, 3 fit a 2 : 1 ratio, 5 a 4 : 1 ratio, 10 a 6 : 1 ratio, 11 a 10 : 1 ratio. For the two last-named high-ratio groups the homogeneity test was positive: $\chi^2 = 4.31$ and 9.75 respectively, $P > 0.80$ and 0.30. The homogeneity tests for the entire frequency series gave for both sexes (expectation 3 : 1) a significant value $P < 0.01$.

Thus we see that the series indicates a mixture of normal and highly divergent ratios, with a considerable amount of transgression. The multimodal aspect of the curve is obviously caused by the presence of different ratios. A 4 : 1 ratio would be expected if a chromosome (the second or another) carried a condition which in the presence of px/px is homozygous lethal, which would eliminate one-fourth of the F_2 px flies. Further, if a lethal combination were produced by homozygosity of the

px chromosome in conjunction with a recombination of something in the X chromosome, a ratio of 6 : 1 might be produced. If, however, the presence of the px chromosome in heterozygous state leads to lethal recombinations with one or more other chromosomes (say, via hyper- or hypoploidy), the lower ratios of 1, 2, 2.25 : 1

TABLE 103

SOME INDIVIDUAL RATIOS non px : px

No.	Type of cross	Ratio non px : one px		Number of flies
		♀	♂	
2076	$(N \times px\ bl)^2$	1.1	1.4	152
2084	$(px\ bl\ blist \times N)^2$	1.6	2.0	218
2287	$(N \times px\ bl)^2$	2.1	1.8	232
2054	$(px\ bl\ blist \times N)^2$	2.4	2.5	217
261	$(\underline{Y} \times px\ bl)^2$	2.8	3.1	67
792	$(px\ bl \times N) \times$ recipr	3.1	3.5	259
770	$(px\ bl \times N) \times$ recipr	3.9	3.6	179
760	$(px\ bl \times N) \times$ recipr	4.3	4.2	105
300	$(\underline{Y} \times px\ bl)^2$	5.1	4.7	106
784	$(px\ bl\ blist \times N) \times$ recipr	5.9	7.7	238

may be produced by elimination of not px classes. Finally, if the second chromosome contained a condition lethal when homozygous and not too closely linked with the px locus, all homozygotes for px might be wiped out in a proper F_2 combination, except crossover individuals. Such a situation would account for the very low px ratios above 6 : 1. (A rough calculation assuming a 10 : 1 ratio puts the

TABLE 104

COMPARISON OF F_2 RATIOS IN FEMALES AND MALES

No.	Type of cross	Ratio non px : one px		Number of flies
		♀	♂	
795	$(px\ bl \times N) \times$ recipr	2.7	3.7	197
793	$(px\ bl \times N) \times$ recipr	2.7	5.9	199
291	$(\underline{Y} \times px\ bl)^2$	2.8	6.1	104
284	$(N \times px\ bl)^2$	2.5	16	170
278	$(N \times px\ bl)^2$	1.8	3.8	209
285	$(N \times px\ bl)^2$	4.3	2.4	203
2079	$(px\ bl \times N)^2$	5.2	3.4	209
252	$(\underline{Y} \times px\ bl)^2$	3.5	2.2	84
301	$(\underline{Y} \times px\ bl)^2$	6.5	2.9	118
493	$(N \times px\ bl) \times$ recipr	4.0	2.4	215

disturbance at a rather long distance from the px locus). These data, then, encourage a search for a homozygous lethal condition in the second chromosome and eventual translocations between this and other chromosomes.

The detailed data lead one step further still. If male and female ratios are compared in the same brood, we find them frequently alike for high as well as for low ratios. A few selected examples are given in table 103. But still more frequently,

males and females show different or highly divergent ratios. The higher ratio may be on the female or the male side, though more frequently on the male. For a few selected examples see table 104.

This, together with the highest ratios occurring only in males, suggests that the X chromosome also is involved. But it cannot be the case of a simple modifier, as in crosses with attached X females the different types just described are also found. Finally, it is to be noted that out of six cases in which the ratio for females was above 5 : 1, two belonged to a cross with y, i.e., had foreign X chromosomes, three belonged to a combination permitting two foreign X, and only one could not contain females with two foreign X.

An explanation can be found if we remember the two- or three-band deficiency next to bs ba and its possible insertion in the X chromosome near facet. An F_2 combination of the homozygous deficiency is likely to be combined in the males with half a normal X = lethal and half a duplicated X = viable, which means a ratio for + : px = 6 : 1. In the females the same might be the case, or, if the father had the duplicated X chromosome, all px daughters might be viable. Unfortunately, no known locus seems enclosed in the deficiency near bs. The rare cases of extremely high ratios in males (e.g., no. 284 : 65 ♂ + 4 ♂ px = 16 : 1) probably require a different interpretation. It happens that one of the cases with highest ratio (no. 284) was present in an F_2 involving X-chromosome markers, and in this case a deficiency for echinus actually was present in one X of the px bl stock (see below). This allows for another lethal class of males except for crossing over. A detailed analysis was not possible, but it suffices to know that the deficiencies and translocations known to occur can account for these ratios in a general way. The important point is the presence of small, genetically demonstrated rearrangements, even though they cannot be located in detail.

h. TESTS FOR TRANSLOCATIONS

We have mentioned above certain facts which suggested that small translocations 1→2 and 1→3 as found in pointed, as well as some transposition in the X chromosome, might be present in px bl. Moreover, one small translocation 2→1 was actually found, which eventually accounted for the facts (see p. 345). The standard Patterson translocation test was thus not expected to produce lethal classes except if small duplications were lethal, which is not probable (see above, p. 319). Table 105 contains some of the data of such tests. All crosses were made with a Patterson stock selected for extreme expression of eyeless. Actually, in the controls there is very little difference between the ey and not ey classes, the ey class sometimes even being the larger one. But in the px bl II crosses, as before in poi crosses, there is such a difference. Looking only at the + and ey class, one might assume that here a part of the ey flies are phenotypically +, as both classes together contain about the same number of flies, e.g., bw and bw ey or e and e ey together. But the extreme difference is found only in the + ey group, not in the others, with the exception of the ♀♀ bw and bw ey in the px bl II crosses, where a huge difference becomes visible. Actually, in a considerable number of individual crosses there were no bw ey females at all; in others, only a single one where ten to fifteen were expected.[12] The obvious explanation is that a third chromosome from px bl II contains a suppressor for ey, as has

[12] Ratios above 8 : 0 and 11 : 1 are significantly different from 1 : 1.

already been discussed for other stocks (see p. 357). The positive tests for this explanation have already been given. The stocks discussed before were all derivatives of px bl. The results are statistically significant. For the Oregon control:

TABLE 105

1-3. Cross: y, bw, e, ey × (N × bw, e, ey). 4. Cross bw, e, ey × (px bl II × bw e ey)

N	♀							
	Patt	bw e	bw ey	e ey	bw	e	ey	+
1. px bl II	105	68	36	82	127	89	69	132
2. px bl 4856	52	51	48	47	60	38	36	83
3. Oregon	68	73	58	62	87	81	73	89
4. px bl II	66	53	58	79	88	83	59	116
N	♂							
	bw e ey	bw e	bw ey	e ey	bw	e	ey	+
1. px bl II	67	80	89	85	102	111	80	135
2. px bl 4856	58	62	48	43	66	65	44	84
3. Oregon	94	123	98	80	85	114	80	123
4. px bl II	57	40	43	54	105	58	37	132

$\chi^2 = 12$ P = 0.10 for ♀♀ and 29, P = <0.01 for ♂♂. For px bl II the values are 80.88 for ♀♀ and 52.61 for ♂♂, which are large deviations from normal, far below P = 0.01. The deviations in the individual classes cannot be said to be confined to the ey group, even though significant differences between the classes are found in the controls

TABLE 106

Percentage of Deviation from Norm = +

	♀						
	Patt	bw e	bw ey	e ey	bw	e	ey
Control	24	18	35	30	2	9	18
Expectation	20	49	73	38	4	33	48
Difference	−4	31	38	8	2	24	30
	♂						
	bw e ey	bw e	bw ey	e ey	bw	e	ey
Control	32	..	20	35	31	7	35
Expectation	50	41	34	37	25	18	41
Difference	18	41	14	2	−6	11	6

also, possibly based upon differential viability in the presence of 0, 1, 2, 3, 4 mutants. In order to compare the px bl II data with the Oregon controls, we might use table 106. The plus type may be taken in both cases as approximating the expected class number. The percentage of deviation from this in the individual classes of the control would measure the loss of viability by accumulation of the recessive markers.

The excess in the experiment after this is deducted would be caused by the respective px bl chromosome present heterozygous in the class, if statistically significant. Aside from the ey situation, this significant difference might show that the different classes have a different viability in different combinations of px bl and foreign

TABLE 107

CROSS: px bl × (B, Cy, D, Sc × px bl)

♀							
B Cy D Sc	B Cy D +	B Cy + Sc	B Cy ++	B + D Sc	B + D +	B ++ Sc	B +++
11	48	4	46	10	37	5	47
♂							
+ Cy D Sc	+ Cy D +	+ Cy + Sc	+ Cy ++	++ D Sc	++ D +	+++ Sc	++++
12	41	4	52	11	35	2	69

chromosomes. As we already know that small deficiencies and duplications of different type may be present in such crosses (but without any reciprocal translocations involving lethal deficient or duplicated classes), a result of this type may be expected.

TABLE 108

CROSS (px bl × bw, e)[2]

No.	♀						♂					
	+ (6)	e (2)	px (3)	px e (1)	bw (3)	bw e (1)	+ (6)	e (2)	px (3)	px e (1)	bw (3)	bw e (1)
2054	46	15	28	5	16	3	36	15	22	6	20	4
2055	52	7	16	4	25	7	39	5	17	3	15	8
2056	31	13	20	7	10	3	23	7	19	6	15	3
2057	17	3	8	..	7	2	22	2	11	1	3	2
2058	50	13	21	10	19[a]	4[a]	32	19	15	2[a]	11	1
2060	39	13	18	4	24	13	39	11	16	6	22	7
2061	30	12	8	6	15	8	28	10	15	3	12	4
2062	31	8	24	6	19	3	32	14	19	5	8	4
Total	296	84	143	42	135	43	251	83	134	32	106	33

χ^2 ♀ = 2.82 P>0.70
χ^2 ♂ = 6.69 P>0.20

[a] Part ♀, all ♂ Bd.

To gain more definite information many other tests were made. Thus, a cross paralleling the Patterson test was made in which, however, the X chromosomes were exchanged, namely, Patterson test: ♀ both X foreign, ♂ X from px bl, cross bw e ey × (px bl × bw e ey) = ♀ one X each from both grandparents, ♂ X from foreign stock. The results are found in the fourth column of table 105. They are very similar to the former ones, except that in some respects the result for ♀♀ and ♂♂ are the reciprocal ones of the former case, e.g., first case: difference bw–bw ey, greater in

♀♀; second case: greater in ♂♂, difference + − ey the same; female class bw e ey in first class large, in second small as in ♂♂. This points to a participation of the X chromosome in the deviations.

Many similar tests with dominant and recessive markers have been made, all of them giving comparable deviations from expectation but none of them of a kind to permit clear-cut conclusions. To show only the type of results without going into details, two more examples may suffice. The cross px bl × (B, Cy, D; Sc, × px bl)

TABLE 109

TEST OF FIT FOR INDIVIDUAL RATIOS FROM TABLE 108

(Ratios and, in parentheses, multiple of standard deviation = $\frac{\text{Dev}}{\text{P.E.}}$. Numbers above 2 = less than 4.6 per cent chance are considered significant. The 1 per cent point is near 2.5. Only tests for more than 50 individuals are included; all others, according to Warwick tables, are insignificant.)

No.	not px : px	not bw : bw	not e : e	+ : e	px : px e	bw : bw e	px : bw	px e : bw e
♀ 2054	2.4 (1.6)	5 (2.9)	3.9 (3.2)	3.1	5.6	5.3	1.8	1.7
♀ 2055	4.6 (2.6)	2.5 (1.3)	5.2 (1.6)	7.4 (3.6)	4.0	3.6	0.6	0.6
♀ 2056	2.1 (2.2)	5.5 (3.0)	2.7 (0.7)	2.4	3.0	3.3	2.0	2.3
♀ 2057	3.6	3.1	6.4	5.7	∞	3.5	1.1	...
♀ 2058	2.8 (0.6)	4.1 (1.9)	3.3 (0.6)	3.8 (1.3)	2.1	4.7	1.1	2.5
♀ 2060	4.0 (1.9)	2.0 (2.9)	2.7 (0.6)	3.0	4.5	1.8	0.8	0.3
♀ 2061	4.6 (2.3)	2.4 (1.2)	2.0 (2.3)	2.5	1.3	1.9	0.5	0.8
♀ 2062	2.0 (2.5)	3.1 (0.4)	4.3 (2.1)	3.9	4.0	6.3	1.3	2.0
Exp.	3 : 1	3 : 1	3 : 1	3 : 1	3 : 1	3 : 1	1 : 1	1 : 1
♂ 2054	2.7 (0.7)	3.3 (0.7)	3.1 (0.3)	2.4 (1.0)	3.7	5.0	1.1	1.5
♂ 2055	3.4 (0.7)	2.8 (0.4)	4.4 (2.2)	7.8	5.7	1.9	1.1	0.4
♂ 2056	1.9 (2.8)	3.1	3.6 (0.8)	3.3	3.2	5.0	1.3	2.0
♂ 2057	2.4	7.2	7.2	11.0	1.0	1.5	3.7	0.5
♂ 2058	3.7 (1.2)	5.7 (3.1)	2.6 (0.8)	1.7 (2.9)	7.5	11.0	1.4	2.0
♂ 2060	3.6 (1.0)	2.5 (1.4)	3.2 (0.3)	3.6	2.7	3.1	0.7	0.9
♂ 2061	3.0	3.5 (0.8)	3.2 (0.4)	2.8	5.0	3.0	1.3	0.8
♂ 2062	2.4 (1.5)	5.8 (3.1)	2.6 (1.2)	2.3	3.8	2.0	2.4	1.2
Σ ♀	3.0 (0.1)	3.2 (1.0)	3.4 (2.1)	3.5 (1.9)	3.4 (1.0)	3.1 (0.3)	1.1 (0.7)	1.0 (0.3)
Σ ♂	2.9 (0.8)	3.6 (2.8)	3.3 (1.6)	3.0 (0.2)	4.2 (2.6)	3.2 (0.6)	1.3 (2.7)	1.0 (0.5)

contains markers for all four chromosomes (Bar, Curly, Dichaete, Scutenick). The latter has—at least in our stock—a poor penetrance, so that it shows in only about ½ of the flies. The result of this cross, expecting 16 equal classes, is shown in table 107. The table shows in both sexes alike the classes containing Sc, and the foreign third chromosome (D) to be about ½ the expected size, i.e., 44 with Sc and 161 without Sc, instead of 102.5 each. But in the presence of the homozygous third chromosomes from px bl the penetrance of Scutenick is more than twice as much inhibited, parallel to the former case with eyeless, namely, 15 with and 214 without Sc, instead of 114.5 each. Tests for a translocation 4→3, or an attachment of 4 to 3, including the cubitus interruptus test, were negative, but a suppressor action was made probable.

Another example showing the difficulties of simple tests in this case is the following: The crosses involve second chromosomes marked with brown, and third ones with ebony, thus furnishing a simultaneous check upon presence, absence, or heterozygous condition of the second px bl chromosome together with the third in the cross (px bl × bw, e)². The normal expectation is 6 + : 2 ebony : 3 plexus : 1 plexus ebony : 3 brown : 1 brown ebony (and eventual crossover flies bw–px). Table 108 shows the results obtained.

In sum total the results look rather normal, thus:

not px : px ♀ 3.01 : 1, ♂ 2.9 : 1
not bw : bw ♀ 3.2 : 1, ♂ 3.6 : 1
non e : e ♀ 3.4 : 1, ♂ 3.3 : 1
(See the χ^2 values for the entire segregation)

An inspection of the individual broods reveals, however, that this result is not based upon normal sampling, but upon the presence of definite groups of deviation in

TABLE 110

SEX RATIOS IN DIFFERENT CROSSES WITH px bl

Cross	No. of broods	No. ♀	No. ♂	Average ratio ♀ : 1 ♂
1. px bl × diff.	168	12470	7030	1.8 : 1 = *ca.* 2 : 1
2. px bl pure ♀♂ not blist.	56	4392	4262	1.03 : 1 = 1 : 1
3. px bl pure ♀♂ blist.	22	1943	1789	1.1 : 1 = 1 : 1
4. px bl pure only ♂ blist.	4	480	495	1 : 1 = 1 : 1
5. px bl pure only ♀ blist.	46	3942	3656	1.1 : 1 = 1 : 1
6. diff. × px bl.	33	1381	1052	1.3 : 1 = *ca.* 4 : 3
7. y × px bl.	15	642	491	1.3 : 1 = *ca.* 4 : 3
Sa.	344	25250	18775	

both directions, as table 109 shows. In this table the ratios of the individual broods for the different segregating classes are calculated. For each ratio based upon more than 50 individuals the fit has been tested by calculating the multiples of the standard error, i.e., deviation from expectation in terms of the standard error. Values above 2 (4.6 per cent probability of chance) or above 2.5 (less than 1 per cent) may be considered as significantly different from expectation. For groups with less than 50 individuals Warwick's tables were used. As all these latter values were not significant (above 0.005), they have been omitted in table 109. We find significant deviations from expectation, both higher and lower ratios four times for females, once for males in the not px : px segregation; three times for females, twice for males in the not bw : bw segregation; three times for females, once for males in not e : e; once each for females and males in the px : px e groups; and four times the sum total was also significantly different. It is hardly possible to analyze these data in more detail. We discussed before, when analyzing the px segregation, the ratios which might be found and how they could be caused. The same line of argument applies in this case, both for the second and the third chromosomes. As far as they go, the data indicate the presence of such conditions as already analyzed above for the silver alleles and, in addition, special features for the second chromosome as discussed earlier with the segregation of plexus.

i. THE SEX RATIO IN CROSSES

The results which indicated a transposition within and translocation from the sex chromosome are first checked by a consideration of sex ratios found in crosses of the px bl line with other stocks. These ratios are entirely abnormal. Tables 110 and 111 contain the results for the different F_1 combinations compared with inbreeding the stock. Table 110 contains the summarized results of 344 broods with about

TABLE 111

NUMBER OF BROODS WITH SEX RATIO n ♀ : 1 ♂

Cross	n																
	0.8	0.9	1	1.1	1.2	1.3	1.4	1.5	1.6	1.7	1.8	1.9	2	2.1	2.2	2.3	2.4
1	2	5	10	6	11	9	10	11	12	6	7	5	8	3	13	9	2
2	7	6	16	12	6	5	1	1	2	..	..	..	..	..	..	..	..
3	1	2	11	3	1	2	1	..	1	..	..	..	..	..	..	..	..
4	1	1	1	1	..	..	..	..	..	..	..	..	..	..	..	..	..
5	4	5	17	9	3	5	..	1	..	..	..	..	1	..	..	..	..
6	2	1	7	5	3	4	3	3	..	1	..	1	..	..	1	1	..
7	1	..	1	2	2	2	4	1	1	..	1	..	..	..	..	..	..

Cross	n																
	2.5	2.6	2.7	2.8	2.9	3	3.1	3.2	3.3	3.4	3.5	3.6	3.7	3.8	3.9	4	4.1
1	..	..	1	3	..	9	..	2	3	2	..	3	..	..	..	1	..
2	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..
3	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..
4	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..
5	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..
6	..	..	..	..	..	1	..	..	..	..	..	..	..	..	..	..	..
7	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..	..

Cross	n															
	4.2	4.3	4.4	4.5	4.6	4.7	4.8	4.9	5	5.3	7	7.8	8	8.7	9.7	∞
1	..	1	2	..	..	..	1	2	..	2	2	1	1	1	2	1

44,000 individuals, reciprocal crosses (1, 6, 7), and the possible combinations within the px bl line as controls. In table 111 the range of variation of the sex ratios of individual broods (average size, 130 flies) is tabulated for each group contained in table 110 (1–7), giving the number of broods found, with the respective sex ratios. The first group comprises 168 F_1 crosses of px bl ♀ with different wild or mutant stocks, excluding balanced or other complex stocks which might effect the sex ratio by themselves. Table 111 shows that very different sex ratios are present in this group, from normal to complete absence of males (∞). The table further shows that these ratios fall into groups, most of which have an obvious meaning. Very rarely, the males are slightly in excess (ratio below 1) and a normal sex ratio is not very frequent, namely, about 17 per cent of all broods (ratio 0.1–1.1) and part of the 1.2 group. There are two overlapping maxima near 1.3–1.4 and 1.6.

Rough calculation attributes about 17 per cent to each. The next mode is near the ratio 2 : 1, with an estimated 12 per cent of the broods. Another obvious mode lies between 2.2 and 2.3 : 1, containing roughly 14 per cent of the crosses. Another mode lies near 3 : 1, with about 10 per cent of the broods. Whether another small group with about 3.5 : 1 exists is not certain. There are a number of broods with a ratio 4–5 : 1, and finally a group between 7 and 9 : 1. There is obviously a considerable similarity with what we have discussed for pointed, and an even clearer multimodal distribution.

This interpretation derived from inspection of the frequency curve was tested statistically. Again all broods with more than 50 individuals were tested with the χ^2 test for an expected ratio 1 : 1. All ratios significantly different ($P<0.05$ and almost all < 0.01) were again tested for expectations 4 : 3, 8 : 5, 2 : 1, 4 : 1, 8 : 1. It is hardly necessary to present all the individual χ^2 values. We tabulate only the results for $P = <0.05$ as limit of significance. There were, in series 1, 147 broods with more than 50 individuals, of which 97 differed significantly from a 1 : 1 ratio; they included all broods beyond a 1.5 : 1 ratio. Of these

5 fit only a 1 : 1 ratio
16 fit only a 1 : 1 or 4 : 3 ratio
29 fit only a 1 : 1 or 4 : 3 or 8 : 5 ratio
5 fit only a 4 : 3 or 8 : 5 ratio
31 fit only a 8 : 5 or 2 : 1 ratio
6 fit only a 2 : 1 ratio
7 fit only a 2 : 1 or 4 : 1 ratio
14 fit only a 4 : 1 ratio
1 fit only a 8 : 1 ratio
1 = 67 : 0 = ∞ fits no other ratio

Arranged according to single ratios:

50 fit a 1 : 1 ratio ranging from 0.8–1.5 : 1
81 fit a 4 : 3 ratio ranging from 0.8–2.0 : 1
96 fit a 8 : 5 ratio ranging from 1.0–2.8 : 1
74 fit a 2 : 1 ratio ranging from 1.4–3.7 : 1
22 fit a 4 : 1 ratio ranging from 2.4–4.4 : 1
2 fit a 8 : 1 ratio ranging from 5.3–8.7

Thus there can be no doubt that the ratios assumed to occur and visible by inspection do actually occur with an expected amount of overlapping. The simplest case, a mother heterozygous for a sex-linked lethal, i.e., an F_1 ratio 2 : 1, is frequent. Only once the most extreme case was obtained, no F_1 ♂♂, i.e., the mother with sex-linked balanced lethals. The other numbers suggest that different male-lethal combinations are formed by certain autosomal combinations with certain X-chromosome conditions. In other words, the px bl line must be differently homo- or heterozygous for coöperating conditions in sex chromosomes and autosomes, and certain combinations of one or both X chromosomes from px bl mother with normal chromosomes from another stock in the heterozygote must be lethal. A number of the ratios have already been found and analyzed for pointed and are assumed to be based here on the same or similar conditions.

Ratio 1 ♀ : 1 ♂ either normal or the same number of female and male classes lethal.

Ratio 1.33 ♀ : 1 ♂, i.e., about 4 : 3. One of four male classes lethal, i.e., mother heterozygous for a nonreciprocal translocation 1→autosome, which produces one male class with deficient X out of four.

Ratio 1.6 ♀ : 1 ♂, i.e., about 8 : 5. Three of 8 male classes lethal. This was shown before to be the result of two such translocations, namely, 1→2 and 1→3.

Ratio 3 ♀ : 1 ♂, i.e., 1 female, 3 male classes lethal. The 3 male lethal classes would be the same as before. The female lethal class, one among four, might be caused by duplication 1→2 and 1→3 with double deficiency in 1. If this is correct, the 1.6 : 1 ratio must have a compensation in the females.

Ratio many ♀ : 1 ♂ might be a case of balanced lethals in the mother with considerable crossing over or a comparable situation (see discussion for pointed, pp. 311 ff.).

Thus we expect that the px bl stock already contains all the small translocations found in pointed or others of the same type, in addition to other abnormal conditions, and that different individuals of the stock may have one or the other or all of these rearrangements.

TABLE 112

FERTILITY TEST

Cross	Fertile among 200	Per cent fertile
♀ px bl A × ♂ Oregon	148	74
♀ Oregon × ♂ px bl A	141	70.5
♀ px bl B × ♂ Oregon	149	74.5
♀ Oregon × ♂ px bl B	134	67
Control Oregon pure	171	85.5

The other control crosses seem to have a simple 1 : 1 ratio with unimodal distribution. The groups numbers 5, 6, 7 were tested statistically by calculating χ^2 for each brood of more than 50 individuals. The results were:

Series 5: 44 broods, 42 fit a 1 : 1 ratio, 2 differ
Series 6: 26 broods, 22 fit a 1 : 1 ratio, 4 differ
Series 7: 14 broods, 11 fit a 1 : 1 ratio, 3 differ

Of the two significantly differing broods of series 5, one had an exact 2 : 1, one a 4 : 3 ratio. The four of series 6 all had good 2 : 1 ratios, and of the three of series 4, two looked like 4 : 3 and one like 2 : 1. The 2 : 1 ratios indicate occasional sex-linked lethals with unimodal distribution. Rare 1 : 3 ratios in the pure-stock crosses would indicate an occasional unbalance within the stock which otherwise must be completely or almost completely balanced, which means that whatever lethal classes may be formed die in equal numbers in both sexes (though different classes may be lethal in the two sexes). If this is true, matings within this line ought to produce fewer offspring than do controls. We first tested the fertility both of males and of females of two different px bl stocks in reciprocal crosses of 200 pairs each under identical conditions. Table 112 contains the results. This shows a small increase of sterility in the px bl crosses.

In order to gain an idea of the amount of lethal classes in this balanced line the following experiment was carried out. From one of the px bl inbred stocks, 20 ♀♀ with blisters and 20 ♀♀ without blisters were crossed to Oregon ♂ (columns 1, 2 of table 113). Further, 20 females from the same bottles were mated to their brothers, and 20 Oregon pairs served as controls. Females of about the same size, all from fresh bottles, were used, all conditions were kept as equal as possible, and the counts were made on the seventeenth day of breeding at 25° ± 1°. Table 113 shows the

result, which is perfectly consistent throughout. It shows, aside from the sex ratios already discussed, that px bl females crossed to wild-type males produce even more offspring than the control (heterosis). The pure px bl produce (only the females are strictly comparable) less than half of the daughters found in the offspring of their cross-bred sisters and about ⅔ of the number in the controls. This is expected when lethal classes are produced in the balanced stock; they might amount to about half of the individuals.

Returning again to table 110, we find as no. 6 the reciprocal cross from no. 1, the difference being that the same autosomal conditions are combined with an always normal X in the male. We expect, therefore, lethal classes only with autosomal combinations not balanced to the foreign X (if any) and, therefore, normal sex ratios, except a few cases of a 3 : 1 ratio, as explained above. Finally, a smaller number of broods is tabulated as no. 7, the crosses of females with attached X chromosomes to px bl males. The males always have only one type of X from the px bl father, the females no such X. A mode near 1.3 was found, which may or may not be significant. Sex ratios are sometimes irregular in attached X crosses which involve *per se* lethal classes (XXX and YY).

j. TESTS FOR TRANSLOCATIONS AND TRANSPOSITIONS

As the greatest complications were expected in the first chromosome, judging from the variation in the F_1 sex ratios reported above, numerous crossover tests were made and repeated at different times. The first group to be reported tests px bl in different combinations with y v f. Instead of using the simple backcross (px bl × y v f) × y v f, different types of F_2 were used which behave like backcrosses as far as the X chromosome is involved but furnish in addition all possible recombinations of the autosomes, including the homozygous condition for the different px bl chromosomes (only the second being marked by px). Thus, many more possibilities of discerning lethal classes are given. The cross $(y\ v\ f \times px\ bl)^2$ thus tests the male X chromosome and furnishes crossover classes in both sexes. The reciprocal cross $(px\ bl \times y\ v\ f)^2$ tests the female X chromosome with only male crossover classes. The double reciprocal cross (px bl × y v f) × (y v f × px bl) again tests the female X chromosomes both with female and with male crossover classes. Tables 114–116 contain the results of this first set of crosses. Table 114 shows at once that special and not simple features are present.

One feature of table 114 is that among the males the forked class is absent five times (against 47 in the reciprocal classes); four times it is very small, with 10 flies as against 50 in the reciprocal classes; seven times it is about one-half the size of the corresponding class (27 to 59); and only three times is it about equal (all values are significant). In two of the male groups without f flies, the v f group is also missing; once, only 1 individual (against 9 y) are present; and twice, one-third to one-half of the reciprocal class are present.

Our former analysis of pointed indicates in which direction an explanation may be found. If a nonreciprocal translocation from the first to the second and third chromosomes of the type found in pointed were present, deficient and lethal male classes could be produced in F_2 with a deficient X recombined with nonduplicated autosomes. The presence of the autosomal duplication depends upon the constitution of F_1, and this again upon absence, heterozygosity, or homozygosity in the px bl

parent. Thus F_2 may be Dp2/+ × Dp2/+, Dp2/+ × +/+, +/+ × +/+, and eventually, the same combinations simultaneously with Dp3 (Dp from T 1→3). With the proper deficient crossover class in the first chromosome, therefore, different ratios of lethal classes are possible, namely, for each of the deficiencies ¼, ½, or all lethal, i.e., ratios of the reciprocal classes of 4 : 3, 1 : 1, or n : 0. In the presence of both deficiencies the ratios are 4.4 : 1, 3.3 : 1, 3 : 1, and enhanced chances for n : 0. Table 114

TABLE 113

FERTILITY TEST

Mating	px bl, blist ♀ × + ♂		px bl, + ♀ × + ♂		px bl pure ♀ and ♂		+ control	
	♀	♂	♀	♂	♀	♂	♀	♂
1	115	53	152	80	51	22	16	17
2	58	17	104	36	92	60	70	84
3	63	28	117	74	36	40	92	112
4	112	52	149	53	27	21	9	26
5	94	71	127	85	36	38	79	78
6	40	39	135	80	21	19	60	88
7	115	56	121	49	25	18	97	93
8	109	25	105	57	17	13	72	61
9	116	72	118	58	36	16	98	83
10	139	71	163	37	67	52	88	87
11	77	44	81	51	84	58	76	46
12	35	12	84	61	13	8	121	98
13	94	32	122	75	12	10	72	70
14	109	70	123	78	88	70	62	55
15	83	35	47	52	84	59	87	99
16	99	64	78	64	57	38	88	83
17	123	74	91	45	94	71	53	56
18	100	50	118	62	24	26	86	70
19	132	90	97	65	69	73	28	26
20	90	88	108	50	46	41	70	63
Sa	2003	1043	2240	1212	979	753	1424	1395
M	100	52	112	61	49	36	71	70

shows that the ratios of ♂ yv–f are rarely more or less normal and might fall into the ratios just mentioned. This would mean that the two deficiencies are located left of f and that different recombinations with the autosomal duplications are found. Statistical tests for the reciprocal male classes yv–f were made for the individual crosses (all fewer than 50 individuals), using Warwick's tables; for the sum totals, by calculating multiples of deviation in terms of standard error, values above 2 (or 2.5) being considered significant. Out of 17 individual cases 8 were significantly different from a 1 : 1 expectation. All but one of these (the 13 : 0 ratio) fitted as well a 3 : 1 as a 4 : 1 ratio, though the 3 : 1 ratio gave consistently lower deviations from expectation. The sum total gave extreme discrepancy from 1 : 1 expectation (d/PE = 12.02) and good fit for 3 : 1 or 4 : 1 (d/PE = 1.39 and 1.25 respectively). This shows the adequacy of the interpretation. The two reciprocal classes y–vf also show discrepancies (see the sum total, table 114, and details,

TABLE 114

TESTS FOR THE X-CHROMOSOMES OF px bl

No.	Cross	♀								♂								Sex ratio ♀ : 1 ♂
		+	y v f	y v	f	y	v f	v	y f	+	y v f	y v	f	y	v f	v	y f	
390	(y v f × px bl blist)²	19	20	11	1	..	28	2	4	15	30	13	3	9	8	1	5	1.0
391	(y v f × px bl blist)²	25	15	6	1	11	7	1	..	14	20	14	2	10	7	2	2	0.9
494	(y v f × px bl)²	20	15	8	7	8	7	3	2	25	25	7	6	9	9	4	3	0.8
396	(px bl blist × y v f)²	75	..	..	..	..	..	..	..	15	19	9	2	9	2	..	3	1.3
406	(px bl × y v f)²	72	..	..	..	..	..	..	..	20	26	9	..	11	..	..	5	1.0
407	(px bl × y v f)²	101	..	..	..	..	..	..	..	27	27	11	..	19	7	2	8	1.0
414	(px bl blist × y v f) × (rec)	12	17	5	7	6	10	3	1	10	9	7	..	9	1	1	1	1.6
433	(px bl blist × y v f) × (rec.)	18	29	9	4	..	6	2	9	12[a]	19	11	7[a]	16	11	1	5	0.9
444	(px bl blist × y v f) × (rec.)	24	22	6	8	15	6	..	1	22	23	7	..	20	11	4	3	0.9
445	(px bl blist × y v f) × (rec.)	24	21	9	9	9	8	1	5	27	21	13	..	7	..	4	5	1.1
448	(px bl blist × y v f) × (rec.)	24	18	14	3	8	15	6	3	17	21	14	3	12	11	2	3	1.1
492	(px bl × y v f) × (rec.)	36	31	7	6	15	18	5	2	18	30	8	4	18	7	1	4	1.3
493	(px bl × y v f) × (rec.)	124 ♀ not classified								20	25	7	6	9	9	4	3	1.5
416	(y v f × px bl) × (rec.)	82	..	..	..	..	..	..	..	15	14	6	2	7	3	1	..	1.7
417	(y v f × px bl) × (rec.)	102	..	..	..	..	..	..	..	18	26	12	6	23	5	1	..	1.1
418	(y v f × px bl) × rec	102	..	..	..	..	..	..	..	13	27	7	3	8	6	2	3	1.5
452	(y v f × px bl blist) × (rec.)	79	..	..	..	..	..	..	..	14	22	7	2	12	3	..	..	1.3
453	(y v f × px bl blist) × (rec.)	87	..	..	..	..	..	..	..	15	25	8	3	9	10	2	1	1.2
										317	409	170	49	217	110	32	54	

[a] soft folded wings.

TABLE 115

CROSSOVER VALUES TOGETHER WITH THE RATIOS OF THE TWO RECIPROCAL CLASSES (EXPECTATION 1 : 1) IN THE CROSSES OF TABLE 114

No.	Crossover				Ratios of reciprocal classes							
	♀		♂		+ : y v f		y : v f		y v : f		v : y f	
	y–v	v–f	y–v	v–f	♀	♂	♀	♂	♀	♂	♀	♂
390	40	21.2	27.8	26.2	1 : 1	1 : 2	0 : 28	1 : 1	11 : 1	4.3 : 1	1 : 2	1 : 5
391	28.7	12.1	29.6	28.2	1.7 : 1	1 : 1.4	1.6 : 1	1.4 : 1	6 : 1	7 : 1	1 : 0	1 : 1
494	28.6	28.6	28.4	22.8	1.3 : 1	1 : 1	1 : 1	1 : 1	1 : 1	1 : 1	1.5 : 1	1.3 : 1
396	....	....	23.7	23.7	.....	1 : 1.3	.....	4.5 : 1	.....	4.5 : 1	.....	0 : 3
406	....	....	22.5	19.7	.....	1 : 1.3	.....	11 : 0	.....	9 : 0	.....	0 : 5
407	....	....	35.6	20.8	.....	1 : 1	.....	2.7 : 1	.....	11 : 0	.....	1 : 4
461	....	....	30.9	20.6	.....	1.4 : 1	.....	1 : 1	.....	1.5 : 1	.....	1 : 1
414	32.8	26.2	31.6	23.7	1 : 1.4	1 : 1	1 : 1.7	9 : 1	1 : 1.4	7 : 0	3 : 1	1 : 1
433	22.1	31.2	40.3	29.9	1 : 1.6	1 : 1.6	0 : 6	1.5 : 1	2.2 : 1	1.6 : 1	1 : 4.5	1 : 5
444	27	18.3	42.2	15.6	1 : 1	1 : 1	2.5 : 1	2 : 1	1 : 1.3	7 : 0	0 : 1	1.3 : 1
445	26.7	28	20.8	28.6	1 : 1	1.2 : 1	1 : 1	7 : 0	1 : 1	13 : 0	1 : 5	1 : 1
448	35.2	28.6	33.3	25.3	1.3 : 1	1 : 1.2	1 : 2	1 : 1	4.3 : 1	4.3 : 1	2 : 1	1 : 1.5
492	33.3	16.7	33.3	18.9	1 : 1	1 : 1.7	1 : 1.2	2.6 : 1	1 : 1	2 : 1	2.5 : 1	1 : 4
493	....	....	39.4	20.2	.....	1 : 1.2	.....	1.3 : 1	.....	3 : 1	.....	1 : 3
416	....	....	22.9	18.8	.....	1 : 1	.....	2.3 : 1	.....	3 : 1	.....	1 : 0
417	....	....	31.9	20.9	.....	1 : 1.4	.....	4.6 : 1	.....	2 : 1	.....	1 : 0
418	....	....	27.5	21.7	.....	1 : 2	.....	1.3 : 1	.....	2.3 : 1	.....	1 : 1.5
452	....	....	25	15	.....	1 : 1.5	.....	4 : 1	.....	3.5 : 1	.....	.....
453	....	....	30.1	19.2	.....	1 : 1.7	.....	1 : 1	.....	2.7 : 1	.....	2 : 1
Σ	30.7	23.6	31.1	22.7	1 : 1	1 : 1.2	1 : 1.5	2 : 1	1.7 : 1	3.6 : 1	2 : 1	1 : 1.8

Standard: y–v = 33; v–f = 23.7.

TABLE 116

SEGREGATION OF PX IN THE CROSSES OF TABLE 113

No.	Ratio not px : px ♀ in classes								Ratio not px : px ♂ in classes							
	+	y v f	y	v f	y v	f	v	y f	+	y v f	y	v f	y v	f	v	y f
390	17 : 2	13 : 7	.....	18 : 10[a]	8 : 3	0 : 1	2 : 0	3 : 1	9 : 6	18 : 12	6 : 3	7 : 1	7 : 6	2 : 1	1 : 0	5 : 0
391	17 : 8	12 : 3	9 : 4	3 : 4	4 : 2	1 : 0	1 : 0	.....	9 : 5	12 : 8	8 : 2	7 : 0	11 : 3	2 : 0	1 : 1	0 : 2
494	13 : 7	13 : 2	5 : 3	6 : 1	5 : 3	3 : 4	3 : 0	2 : 0	18 : 7	19 : 6	8 : 1	6 : 3	6 : 1	5 : 1	3 : 1	3 : 0
396	57 : 24[b]	.....	.....	.....	.....	.....	.....	.....	9 : 6	15 : 4	5 : 4	0 : 2	7 : 2	2 : 0	.....	3 : 0
406	49 : 23[c]	.....	.....	.....	.....	.....	.....	.....	16 : 4	21 : 5	6 : 5	.....	7 : 2	.....	.....	3 : 2
407	69 : 32	.....	.....	.....	.....	.....	.....	.....	14 : 13	18 : 9	15 : 4	5 : 2	9 : 2	.....	1 : 1	8 : 0
461	73 : 19	.....	.....	.....	.....	.....	.....	.....	13 : 9	11 : 4	6 : 2	6 : 3	6 : 0	2 : 2	2 : 0	1 : 1
414	10 : 2	10 : 4	4 : 2	9 : 1	3 : 1	5 : 2	2 : 1	1 : 0	?	8 : 1	8 : 1	?	5 : 2	.....	?	1 : 0
433	17 : 1	21 : 8	.....	4 : 2	6 : 1	4 : 0	2 : 0	7 : 2	?	16 : 3	14 : 2	9 : 2	11 : 0	6 : 1	1 : 0	4 : 1
444	17 : 7	16 : 6	12 : 3	6 : 0	5 : 1	6 : 2	.....	0 : 1	14 : 8	21 : 2	17 : 3	9 : 2	6 : 1	.....	3 : 1	3 : 0
445	17 : 7	17 : 4	9 : 0	6 : 2	7 : 2	6 : 3	1 : 0	4 : 0	20 : 7	18 : 3	5 : 2	.....	9 : 4	.....	4 : 0	3 : 2
448	15 : 9[d]	12 : 6	6 : 2	10 : 5	12 : 2	2 : 1	4 : 2	3 : 0	9 : 5	16 : 5	9 : 3	8 : 3	10 : 4	3 : 0	1 : 1	3 : 0
492	29 : 7	26 : 5	11 : 4	12 : 6	5 : 2	6 : 0	5 : 0	1 : 1	13 : 5	22 : 8	18 : 0	4 : 3	6 : 2	4 : 0	1 : 0	3 : 1
493	.....	.....	.....	.....	.....	.....	.....	.....	15 : 5	20 : 5	16 : 3	12 : 3	9 : 3	1 : 3	1 : 0	2 : 1
416	62 : 20[e]	.....	.....	.....	.....	.....	.....	.....	11 : 4[f]	14 : 0	6 : 1	3 : 0	5 : 1	1 : 1	1 : 0	....
417	77 : 25[g]	.....	.....	.....	.....	.....	.....	.....	13 : 5	19 : 7	17 : 6	5 : 0	8 : 4	3 : 3	0 : 1	....
418	74 : 28	.....	.....	.....	.....	.....	.....	.....	10 : 3	21 : 6	4 : 4	4 : 2	5 : 2	3 : 0	1 : 1	2 : 1
452	57 : 22[h]	.....	.....	.....	.....	.....	.....	.....	11 : 3	20 : 2	11 : 1	0 : 3	6 : 1	2 : 0	.....	....
453	59 : 28[i]	.....	.....	.....	.....	.....	.....	.....	10 : 5	20 : 5	6 : 3	7 : 3	6 : 2	3 : 0	2 : 0	0 : 1
Σ	729 : 271	140 : 45	56 : 16	74 : 31	55 : 17	33 : 11	20 : 3	21 : 5	214 : 90	329 : 95	185 : 50	92 : 32	139 : 43	39 : 12	23 : 7	44 : 12
	2.7	3.1	3.5	2.4	3.2	3.0	6.7	4.2	2.4	3.5	3.7	2.9	3.3	3.3	3.3	3.7
d/PE for Σ	2.3	0.25	0.81	1.69	0.4	0	2.1	0.68	2.76	1.8	2.01	0.3	0.76	0.48	0.63	0.92

[a] All extreme
[b] 2 blist.
[c] 2 blist.
[d] 4 blist.
[e] 5 blist.
[f] 1 blist.
[g] 3 blist.
[h] 8 blist.
[i] 4 blist.

table 115) in favor of the y class. The ratio 217 : 110 is significantly different from 1 : 1 (d/PE = 8.9). This indicates the location of one of the deficiencies between y and v and probably nearer to yellow. Correspondingly, we find here many more low ratios, but also the high ratios up to n : 0 for y : vf ♂. Altogether, the facts for males agree with the expectation and the presence of the same or similar translocations 1→2 and 1→3 as found in poi.

In the females we may expect normal ratios because one of the X always contains the normal loci. The numbers are smaller; they are, leaving aside the first cross no. 39, for yv : f = 64 : 45 = 1.4 : 1; (d/PE = 2.86) for y : vf = 72 : 77 = 1 : 1.

But this cannot be the entire solution. F_1 males clearly cannot survive with a deficient X without autosomal duplication (cross px bl × N). Therefore either all F_1 males must have been Dp/+ (Dp 2 or 3 or both), or in the X chromosome the formerly studied transpositions of the same loci must have been present to compensate for the deficiencies. The normal F_2 male class ought to answer this question. If it contained the deficiency (or deficiencies) its ratios ought to be the same as in the f class, which is not the case. The ratios + : yvf ♂♂ are in most cases normal, but sometimes are as 1 : 2. But this 1 : 2 ratio or the normal ratio does not coincide with the same ratio for yv : f ♂. Therefore another complication must be present, which might well be the transposition. In view of the long distances involved and the few markers, a further inquiry will be useless for this peculiar cross. The crossover values (see table 115) do not contain any pertinent information, but the summarized ratios for + : yvf, in which a lower viability of the multiple recessive chromosome ought to work in favor of the + groups is 317 : 409 with a highly significant d/PE = 5.08.

We turn now to the abnormal brood no. 390 (first in tables 114–116), which contains no y class among the females, whereas the reciprocal class v f contains 28 females. The high number of this class—compared with other broods of about the same size,—together with the high crossover value 40 (standard 33), demonstrates that this is not a normal feature. As table 116 shows, all the 10 px females among 28 females exhibit an extreme plexus formation, which otherwise occurs only in 3 more individuals among the hundreds of plexus flies. We shall see later that such an extreme px may characterize an ec deficiency. The whole situation points out that these excess v f females are actually the missing f ♀ with a vermilion deficiency. They turned out to be sterile (as are the ec deficiencies). This prevented further analysis. This is to be regretted, as other features were present which require a very complicated situation, e.g., all 10 extreme px females must have been the deficiencies. But where are the other px segregants? The y class is here completely missing, but the other classes containing y are normal. No explanation covering all these facts can be offered, and a similar result did not occur again. It is possible that the missing yellow females are contained in the relatively large yv class, i.e., y and v–Df. But here no extreme px was found. Unfortunately, the yv class had not been tested further. We shall see below that an ec deficiency has been found in the stock. Thus all we can say is that additional abnormalities may be present in px bl involving loci of the X chromosome and also px.

In these crosses the second chromosome of px bl was marked with px bs, which might furnish information concerning the supposed 1→2 translocation. Table 116 contains the data for the px segregation in the different crosses and classes found

in table 114. Though some regularities are visible, e.g., in both sexes lower ratios for + and vf than for the reciprocal y v f and y, no clear conclusion can be drawn. The statistical test (see lower end of table) shows only few ratios which might be significantly different from a 3 : 1 ratio. They are the + and v classes in females and the + y classes in males. This does not allow of definite conclusions. We notice again, as before, that blistering occurs only in normal females with two X from px bl.

TABLE 117

(px bl × X^7) × X^7

Class	♀	♂	d/PE
+	42	24	3.29
y w ec cv ct v f	25	2	16.8
y	..	..	....
w ec cv ct v f	..	..	....
y w	5	1	
ec cv ct v f	..	..	
y w ec	2	4	
cv ct v f	7	..	
y w ec cv	6	5	All left of
ct v f	5	..	v 21 : 14 = 2.0
y w ec cv ct	8	4	All right of
v f	10	1	v 38 : 15 = 7.72
y w ec cv ct v	13	6	
f	13	4	
y w f	2	..	
y w ec cv ct f	1	..	
v	3	1	....
ec cv	1	..	....
cv ct	1	2	....
cv ct v	4	7	....
ec cv ct	..	1	....
ct v	3	..	....
y w ec v	1	..	....
	152	56	9.8

Out of many crosses made with more first chromosome markers, only one gave a result comparable to those contained in table 114, a cross with seven recessive markers (X^7). As table 117 shows, almost ¾ of the males were lethal. In the + class about half of the males are missing, in the X ple class most of them. Further, all males are missing when the right half of the X chromosome, including cv, is replaced, and most of them if v f or f is present. Clearly, a region of the X chromosome near vermilion is needed for male survival in the presence of the left half of the original X. The last column of the table contains the statistical tests for an expected 1 : 1 ratio with significant values except for the crossover classes left of v. A transposition alone does not explain all data, which suggest, as before a combination of a transposition with translocations 1→autosomes.

When we tried to analyze this condition further, it turned out that the long-inbred stocks no longer contained the same abnormalities, which it seems had been inadvertently selected out while other work was at the fore. A series of 44 F_2 be-

tween px bl and N (an X ple stock with 9 markers) gave more normal than abnormal sex ratios, but never gave the same features as reported above. Table 118 summarizes only the grand total since the individual broods do not furnish any decisive information. The absence or small number of multiple recessive classes is obviously based on viability. Taking this into account, reciprocal classes are about equal.

TABLE 118

FORTY-FOUR CROSSES (px bl × X^9) × (X^9 × px bl)

Class	Sum total ♀	Sum total ♂	d/PE
+	1703	1360	9.2
X^9	229	217	0.8
y	48	65	2.2
w ec cv ct v m g f	....	....	....
y w	118	117	0.2
ec cv ct v m g f	2	1	....
y w ec	221	161	4.5
cv ct v m g f	136	66	7.3
y w ec cv	173	194	1.6
ct v m g f	153	134	1.8
y w ec cv ct	253	240	0.8
v m g f	280	224	3.7
y w ec cv ct v	73	48	3.2
m g f	62	65	0.3
y w ec cv ct v m	60	30	4.7
g f	114	113	0.2
y w ec cv ct v m g	62	54	1.1
f	260	182	5.5
All multiple c.o. y not w	11	25	P = 0.029
All multiple c.o. w not y	3	3	P = 1.0
multiple c.o. w–ec	110	53	6.7
multiple c.o. ec–cv	121	120	0
multiple c.o. cv–ct	109	110	....
multiple c.o. ct–v	142	115	2.4
multiple c.o. v–m	101	59	4.9
multiple c.o. m–g	94	85	1.1
multiple c.o. g–f	197	180	1.2
Total no. of individuals	4835	4021	12.8

The statistical tests show significant aberrations from a 1 : 1 sex ratio in favor of females (last column, table 118) in the + class; further, among single crossover classes in y w ec, ec ct v m g f, v m g f, y to v, y to m, f; among multiple crossover classes, in those with a break between w–ec, ct–v, v–m. The exact ratios are not relevant, as they are based upon many broods which probably were not alike genetically since the px bl parent might have introduced any of the aforementioned abnormalities or none. The regions involved in the aberrant ratios are those mentioned before. Here, likewise, a simple explanation is out of the question, and both transpositions within the first chromosome and translocations into an autosome are required to account for the facts. A check for the second chromosome marked by

px was made, but without clear results. Crossing over is rather normal except for a rather high value in the ec–ct region.

This experiment furnishes some additional data for problems already discussed, namely, the segregation of blistering and plexation. The results are in conformity with those presented above and are as follows. Out of 44 broods only 7 contained altogether 28 ♀ 1 ♂ blistered. These were found exclusively in the + class, though about ⅓ of the females and ¾ of the px males belonged to the not + classes. The

TABLE 119

SEGREGATION OF px IN TABLE 118

	Ratio not px : px															
	below 1 : 1	1–2 : 1	2–3	3–4	4–5	5–6	6–7	7–8	8–9	9–10	10–11	11–12	12–13	14	17	27
Cases ♀	1	5	9	16	5	3	2	..	..	..	..	..	..	..	..	..
Cases ♂	..	2	7	9	3	3	9	2	2	..	..	1	1	1	1	1

presence of the entire px bl X chromosomes and therefore probably of more than one locus is needed for the blistering effect. The range of variation of not px : px ratios in 42 F_2 is shown in table 119. The ratios closely resemble those which we tabulated before (see table, p. 456) for other F_2 crosses as a whole and therefore will not be analyzed further.

A further attempt was made to localize the small translocations expected to be present in px bl on the basis of the foregoing data by crossing px bl on a rather large scale with a number of available stocks marked with many recessives in two

TABLE 120

(px bl × a sp) × a sp

	♀	♂
+	465	470
a sp	449	246
a.	30	21
sp	31	23

Crossover, 6.2 ♀ 5.8 ♂; stand., 7.8.

or three chromosomes. The tedious counts gave practically no results because lethality or unviability of classes with many homozygous markers in more than one chromosome obscured any possible clear information; and further, the numerous classes—in one experiment with 3 marked chromosomes, 84 discernible classes—could not contain sufficiently large numbers to give significant information. Thus, these data tend to show only the difficulty of genetically testing small transpositions and translocations not involving known loci and probably not lethal in duplicated or deficient condition except for deficiencies in the male first chromosome.

More successful were tests for marked regions in one chromosome alone. One test which was carried out in a series of simultaneous crosses for the right end of the second chromosome marked with a sp gave very similar results to those previously

described for pointed, though pointed is not present, as is shown clearly by the lack of sp suppression. The ratios are found in table 120. The a sp sex ratio of 2 : 1 suggests again the presence of a small translocation1→2 into the a–sp region. Years later, many more such tests were made with the same or different markers. Nothing

TABLE 121

(px bl × h cu) × h cu

	♀	♂	Sex ratio
+	296	269	1.1 : 1
h cu	180	80	2.3 : 1
h	69	56	1.2 : 1
cu	57	55	1 : 1
	602	460	1.3 : 1

comparable was found, showing, as before, that within the stock the presence of the small rearrangements was in constant flux. We shall return to the second chromosome later.

Very similar were the results for the third chromosome. In a considerable number of crosses no lethal action for males was found which would point to a nonreciprocal translocation 1→3. But sometimes a positive result appeared. Thus in a set of

TABLE 122

(px bl × e tx) × e tx

	♀	♂	Sex ratio
8 normal broods:			
+	376	336	1.1
e tx	204	182	1.1
e	96	84	1.1
tx	76	69	1.1
6 broods with obviously the translocation 1→3:			
+	335	257	1.3
e tx	153	69	2.2
e	64	32	2.0
tx	62	36	1.7

crosses (px bl × ru ve h th) × ru ve h th, perfectly normal results appeared among 470 ♀ 542 ♂, but for unusually high crossover values (e.g., ru–ve standard 0.2, obtained 2.4). But in another series exploring the region near h the result was different, as table 121 shows. The table shows one-half of the males with the foreign third chromosome lethal but the h cu region not involved. In pointed we had found a region beyond the ebony region, far to the right in the other arm, responsible. Actually, the same region turned out to be decisive here, too. The following results obtained from a series of crosses with marked third chromosomes, including ebony and made in different years, are given in table 122.

The latter group in table 122 indicates the location of the insertion to the right of ebony. Another series testing the region to the left of ebony is in agreement,

namely, (px bl × ru h cu) × ru h cu, curled (cu), being 20 units left of e. The cu-containing class may therefore be without ebony and the region right of e by double crossover (table 123). Altogether, we have reason to assume that the same or similar translocations and transpositions as were found in poi are distributed also within the px bl stock.

TABLE 123

(px bl × ru h cu) × ru h cu

	♀	♂	Sex ratio
5 normal broods:			
+	121	151	0.8
ru h cu	56	52	1.1
All c.o. no cu	80	85	0.9
All c.o. with cu	53	47	1.1
6 broods with translocation:			
+	244	231	1.1
ru h cu	139	73	1.9
All c.o. no cu	183	171	1.1
All c.o. with cu	100	74	1.4

TABLE 124

px bl Crosses Showing an ec-Df

No.	Cross	♀+	♂	♀ec	Remarks
1708	px bl blist × X^9	79	51	1	ec with short bristles, sterile
1711	px bl blist × X^9	17	9	2	All ec short bristles, sterile
1715	px bl blist × X^9	91	65	6	All ec short bristles, sterile
585	px bl × X^6	20	15	1	All ec short bristles, sterile
....	22 more similar crosses.	Normal		..	
733	(px bl × X^6)^2 F_1 no ec	65	52	1	♀ ec extreme px and bb
	Many the same	Normal		..	
748	585^2	130	30	2	2 ♀ ec, 1 extreme px and bb and blist, 1 not px
749	585^2	82	43	1	♀ ec extreme px and bb
750	585^2	56 (8)[a]	23	22	4 ♀ ec extr. px bb, 18 not px
751	585^2	52 (5)	30	6	5 ♀ ec extr. px bb, 1 not px
752	585^2	Normal		..	
753	585^2	53 (6)	37	20	2 ♀ ec extr. px bb, 18 not px
754	585^2	131 (25)	53	1	1 ec bb but not px
756	585^2	58	2	2	Very few males. 1 ♀ ec extr. px bb, 1 not px
490	(px bl × X^6)^2 F_1 no ec	96 (19)	68	11	All ♀ ec extr., px bb
491	(px bl × X^6)^2 F_1 no ec	101 (21)	50	4	All ♀ ec extr., px bb

[a] No. in parentheses px.

k. Deficiencies in px bl

As the salivaries showed that quite a number of small deficiencies were present in the px bl stock, the regions in question, as well as many others (about 200 loci), were tested for the presence of deficiencies at known loci, and the tests were also carried on another generation to test deficiencies by translocation. The results were always negative, with one exception, the echinus locus (1, 5.5). Deficiencies for this locus

were always found when a number of crosses involving the marker ec were made. Table 124 contains all the cases found in F_1 and F_2.

In about 15 per cent of the crosses in which a check for an echinus deficiency in F_1 was made, a few ec females appeared, altogether 10 among 207 normal sisters. All of them had short bristles like bobbed or Minute (no bb was present in the test stocks) and were sterile, though they lived up to two weeks in the mating bottles. F_2 from normal broods gave, in a considerable number of cases, only normal offspring, but once (no. 733) an ec female appeared, bobbed, sterile, and extreme plexus. From one of the F_1 which had contained one echinus female (no. 585), 8 F_2

TABLE 125

(px bl × sc ec ct) × (sc ec ct × px bl)
(♀ only)

Class	No. 760	No. 761	No. 763	No. 764	Σ
+	42	37	40	38	151
px	10	8	8	8	34
sc ec ct	19	6	8	7	40
sc ec ct px	3	1	..	1	5
sc	1	..	..	1	2
sc px	..	..	1	..	1
ec ct	1	..	3	..	4
ec ct px	1	1	1	1	4
sc ec	11	13	1	6	31
sc ec px	2	..	2	5	9
ct	6	4	1	3	14
ct px	1	1	1	..	3
ec	5	1	5	5	16
ec px	3	2	6	4	15
sc ct	..	..	..	..	..
sc ct px	..	..	..	..	..

were bred from normal females. Seven of these contained ec females, five only a few, comparable to the F_1 result, but three about as many as there were males. In the latter cases the majority were not px, though Minute; when only a few ec females were present these were more frequently extreme px, namely, 8 px, 3 not px, though only ¼ px flies ought to be found in all classes. In two more F_2 in which F_1 had not contained ec, 15 among 221 females were ec, M, extreme px. Again the ec females turned out to be sterile.

Where the ec deficiency is present it ought to show up also in such crossover tests which give crossover females. If, for example, the test is made with sc ec ct, few crossovers sc–ec (5.5 per cent) are expected, and not many double crossovers (0.8 per cent). An excess of the ec class among the females without an excess of the reciprocal class will indicate the ec deficiency. (The reciprocal class would contain one-half of the normal crossovers). Table 125 gives such a test for females, indicating also the px segregation, namely, (px bl × sc ec ct) × reciprocal, nos. 760–764. F_1 did not show any ec deficiency; all F_2 are sister broods. The table shows at once the large ec and ec px class, the reciprocal class being absent (only 0.8 per cent of both expected). In three cases the sc ec class is too high as compared with the reciprocal ct class, presumably by containing also sc individuals with ec deficiency.

We shall not discuss here the px numbers except to point out that one-half of the ec class is plexus. By way of contrast we add as table 126 a similar F_2 in which no ec deficiency is involved, using as markers y w ec f.

Table 124 shows that in F_1 the ec-deficient flies appear only in small numbers, far from one-half. As no females are missing and the deficient flies are perfectly viable, though sterile, there is no reason to assume that the mothers were heterozy-

TABLE 126

(px bl × y w ec f) × (y w ec f × px bl)

Class	No. 778		No. 776		No. 775		Total	
	♀	♂	♀	♂	♀	♂	♀	♂
+	41	29	24	5	29	25	94	59
+ px	10	6	7	1	8	4	25	11
y w ec f	25	32	16	18	18	22	59	72
y w ec f px	8	8	4	1	4	2	16	11
y	..	1	1	1	..	..	1	2
y px	..	1	..	..	..	..	..	1
w ec f	..	..	..	..	..	1	..	1
w ec f px	..	..	..	..	..	..	..	..
y w	..	..	..	..	..	..	..	..
y w px	..	..	..	..	..	..	..	..
ec f	1	..	..	..	..	..	1	..
ec f px	3	..	..	..	..	..	3	..
y w ec	25	8	22	2	19	5	66	15
y w ec px	2	1	3	1	4	3	9	5
f	24	15	19	14	22	20	65	49
f px	2	4	3	4	7	4	12	12
ec	..	..	..	..	..	1	..	1
ec px	..	..	1	..	..	..	1	..
y ec	..	..	..	..	1	..	1	..

The reduced male classes have already been discussed with the X^9 crosses.

gous for the deficiency. Further, an F_1 which had contained only one deficient female produced in F_2, from normal females, seven out of eight times F_2 broods with ec-deficient daughters. In four cases the numbers were small, as in F_1, and in three cases as many daughters as there were sons showed the deficiency. To this ought to be added the two sister F_2 broods (table 124) and the four sister F_2 (table 125), all containing ec-deficient females. These facts indicate that as a rule the ec deficiency is covered by a duplication, which indicates that a small section of the first chromosome containing ec is translocated or transposed somewhere, and that this translocated piece may be removed by crossing over in F_1 or F_2, or by recombination, or both.

Looking at the ratios encountered in tables 124–125, we find what looks like three groups, namely, (1) only a small percentage of ec flies, (2) about as many ec females as the number of males, (3) about one-eighth of ec females. The numbers are:

1) 8 broods with 625 ♀ 303 ♂ 9 ♀ Df = cr. 2 per cent
2 *a*) 3 broods with 239 ♀ 162 ♂ 23 ♀ Df
2, *b*) 4 broods with 191 ♀ (♂ not counted) 31 ♀ Df } = cr. 8 ♀ : 1 Df (7 : 1 ?)
3, *a*) 2 broods with 109 ♀ 60 ♂ 42 ♀ Df = 2.6 ♀ : 1 Df
3, *b*) 1 brood with 58 ♀ 2 ♂ 2 ♀ Df = 3.3 per cent Df

This grouping also shows remarkable sex ratios, namely, about 2 : 1 in the first group, 1 : 6 in the second group, 2 : 5 in the third (*a*) group, and 30 : 1 in the third (*b*) group.

The ratio ♀ : ♀ Df = cr. 3 : 1 found in the third (*a*) group is explained if the non-deficient mother was heterozygous both for the ec-Df and the transposition into an autosome, and the father likewise (simplex for ec-Df). This requires lethality of the homozygous deficiency, but not of the homozygous transposition. If the mother was constituted as described, but the father was heterozygous for the autosomal transposition but did not contain the ec deficiency, ⅛ of the daughters should be deficient. The series of F_2 from the same F_1 in table 125 contains both types, as expected. The transposition is not expected to be in the second chromosome, since in all groups the deficiency recombines with px, i.e., both second chromosomes from px bl. We must therefore expect it to be in the third or fourth chromosome. In all groups assumed not to show a 7 : 1 segregation of the deficiency the segregation of px is as irregular as in the normal class and clearly independent of the deficiency (table 124). But in the group which we interpreted as a 7 : 1 segregation for the deficiency twice all deficiencies were px (15 individuals), twice half were px (16 : 15), and once 5 among 6. This can hardly be a chance result. The differential feature of this group is that the father does not contain the ec deficiency. It follows that in this case daughters heterozygous for ec-Df require the presence of two second chromosomes from px bl. The X chromosome introduced by the father must therefore contain something which is viable only or mostly in the presence of two X chromosomes from px bl stock, and the same thing must not be present in the X containing the deficiency. A translocation between 1 and 3 must somehow be linked with the ec-Df so that both are not present simultaneously in the same X. In view of the rarity of the deficiency and its sterility, no attempt at further analysis of this and some other problems presented by this Df was made.

The plexation in females with the ec-Df (uncompensated) was always extreme. There is a possibility (as we had assumed originally) that some connection with the abnormalities near the px and bs loci (see above) are responsible; but we did not succeed in establishing it. Possibly the high plexation is only an enhancing effect of the deficiency.

There remain still to be explained the F_1 and F_2 groups with only 2–3 per cent deficient females. F_2 from such a cross (748–756, table 124) shows that many F_1 flies were heterozygous for the deficiency. If the mother had been homozygous for the translocated ec locus, all F_1 ought to have been normal. The small percentage of deficient females could thus not be explained. There is a possibility that these were survivors from an otherwise female lethal class, but we are at a loss to explain the production of such a class. The sterility of the deficient females did not encourage further search.

There remain the sex ratios, which are not different in principle from those found before, though the high ratios are more frequent. There is a male lethal ec–Df class involved which alone would not explain the ratios in the presence of the translocation of the ec locus into an autosome, though its addition to the other features producing male lethal classes might.

The segregation of F_2 px females is also remarkable. In the six F_2 where it was registered the segregation was as follows.

750.	78 :	12 = 6.5	d/PE = 2.89
751.	58 :	10 = 5.8	2.91
753.	73 :	8 = 9.1	4.58
754.	132 :	25 = 5.3	3.82
490.	107 :	30 = 3.6	1.17
491.	105 :	25 = 4.2	2.0
Total	553 :	110 = 5	

This is far from a 3 : 1 ratio and is in almost all instances significant. Lethal female classes in the presence of both second chromosomes from px bl are possibly involved. There is again some relation between the translocation ec→autosome and the not directly involved second chromosome, as we saw with respect to the linkage of plexus and the deficiency in some crosses, a relation difficult to visualize in detail.

Finally, one more peculiarity of these crosses should be mentioned. We remember that blistering is extremely rare in the F_2 crosses with px bl, that with few exceptions, it appears only when both X chromosomes from px bl are recombined, and that the extremely rare crossover cases indicate a locus at the left end of the X as responsible for blistering, a locus which normally must be involved in a peculiar system of balance to explain the behavior of the px bl stock. Now in one of the F_2, no. 748, in which the females could contain only one of the px bl first chromosomes, a large number of blistered flies, all high-grade px, appeared among the px flies, and all the px–ec flies were simultaneously blistered. This suggests a further relation of the rearrangement under discussion to the blistering effect, again very hard to understand or to analyze in detail.

1. DOMINANCE AFFECTING SMALL TRANSLOCATIONS IN px bl

In our search for deficiencies at the suspected loci we found two more strange cases. In one cross (px bl × X^v)^s, among 118 females, normal according to expectation, one female v was found. This was crossed to y v f males. One chromosome of the female was derived from X^v or a part of it after crossing over; the other was a pure px bl X chromosome. Therefore either the latter had mutated to v, or was deficient for v, or the recessive v had become dominant. In the first case, daughters as well as sons ought to be v (with the addition of eventual y and f in the females and grandmaternal as well as maternal crossover classes in the males). In the case of v deficiency, daughters ought to be as before and sons all v and ½ missing (also crossover types as before or ½ + if v deficiency were viable in the males). The actual result was:

24 ♀ +, 6 with abnormal abdomen	9 ♂ cv ct v m g f
12 ♀ v	2 ♂ cv ct v m g
24 ♀ v f 8 with abnormal abdomen	1 ♂ v
2 ♀ f	1 ♂ f
16 ♂ +	

This excludes both deficiency and mutation. As the main classes of the daughters were + and v f and the males had cv ct v m g f, the constitution of the mother was obviously $\frac{+}{\text{cv ct v m g f}}$. Half of the males were missing, and as + and cv ct, etc., were present in equal numbers in the males, the missing males were in both classes of X chromosomes, i.e., based upon an autosomal condition like deficiency or dupli-

cation by translocation. Approximately one-fourth of the + and v f females had abnormal abdomen. These might eventually represent the abnormal classes, viable in the female. The two crossover classes v and f are very unequal, but together they give a normal crossover percentage. If, however, a part of the v females were actually heterozygotes with change of dominance, they might have been based upon an autosomal recombination involving a translocation with an effect like Dubinin's cubitus interruptus. Unfortunately, this was not realized in time and no further tests with the v females were made. The facts are therefore only of importance as a case of rare survival of a combination which involves autosomes and the v region.

TABLE 127

Class	No. 1032	No. 1033	No. 1034	No. 1035	No. 1036	No. 1031 (mother px)	No. 1058
♀ y w.....	..	..	16[a]	..	..	..	25
y	..	..	1	..	..	..	1
w.....	40	..	..	..	..	..	..
+.....	50	89	22[b]	113	70[c]	32[d]	30
♂ y w.....	..	..	25[b]	..	..	..	20
y	..	..	1	..	..	..	..
w.....	20[f]	..	..	..	..	..	..
+.....	28[g]	74	18[h]	35	29[i]	29[j]	23

[a] 7 bobbed.
[b] 10 bobbed.
[c] 1 ♀ soft blist, 1 ♀ small eye.
[d] ½ bobbed.
[e] 3 bobbed.
Bobbed means phenotype only.
[f] 1 ♂ notch.
[g] 2 ♂ spread.
[h] 2 bobbed.
[i] 11 ♂ dwarf, soft, part spread.
[j] + bobbed.

The abnormal abdomen turned out to be somewhat genetic, as it reappeared in two grandchildren bred from abnormal abdomen, though never in later generations.

Another isolated case of importance was found for the left end of the X chromosome. Among numerous F_1 between px bl and different combinations involving the y and w loci the following result was obtained once:

No. 591: px bl × y w 71 ♀ 58 ♂ + 1 ♀ w not y

The exceptional w female was mated to a normal brother (which carried the px bl X) and produced:

No. 782: 127 ♀ + 45 ♂ +, 61 ♂ w

The white mother therefore was no homozygous mutant and had no deficiency for white, and she must have carried a suppressor for y. As the decisive feature must be present among the + females, seven of them were mated to y w stock males. The result is set forth in table 127.

The table shows twice ½ y w and ½ + females and males and a normal sex ratio. The mothers, daughters of the exceptional w females, were ordinary heterozygotes for y w and therefore the exceptional w females had had one y w chromosome. (There are also two crossover y females and one white male.) Four times only were normal females and males found in good-sized broods, two of which had a normal sex ratio and two a sex ratio of 3 : 1. The other X chromosome of the exceptional w female had therefore been normal and the constitution must have been just y w/ + +, as if no w had been visible. But one of the broods contained ½ w ½ + in

both sexes and only half as many males as females. This result would be obtained if the mother were +/y w plus autosomal suppressor (duplication) for yellow. But this still does not explain why the F_1 heterozygous grandmother, proved to have been +/y w without a w–Df, was phenotypically white, though this might have been a kind of Dubinin effect, dominance of w in the presence of a translocation with a break near w and containing the y locus. Therefore both white and red pairs from 1032 were bred. The results are shown in table 128.

White pairs produced only white daughters, but both yw and w sons, once in equal numbers, twice approximately 3 y w : 1 w, which agrees with the interpretation just derived. Red parents produced only normal daughters and half y w sons plus a few crossovers. The mother thus was heterozygous for y w and the

TABLE 128

1190–92 = 1032[2] white, 1193 = 1032[2] +

Class	No. 1190		No. 1191		No. 1192		No. 1193	
	♀	♂	♀	♂	♀	♂	♀	♂
w	23[a]	5[b]	50[c]	10[d]	48[e]	15[f]	..	..
w px	9	5	..	..	..	..	..	..
y w	..	9	..	35	..	25	..	30
y w px	..	2	..	..	..	..	..	..
+	..	..	..	..	..	..	83[g]	22[h]
y	..	..	..	..	..	..	..	1
w	..	..	..	..	..	..	..	1

[a] 2 soft wings, 1 scalloped.
[b] 2 ♂ spread, 3 soft.
[c] 7 soft.
[d] 6 soft, 4 spread.
[e] 6 soft.
[f] 5 soft.
[g] 16 soft, 1 spread.
[h] 16 soft, 2 spread.

translocation producing the w dominance effect was absent in both parents. Again, a considerable number of abnormal individuals occurred.

The scalloped white ♀ of 1190 was crossed to a tester ♂ and produced half w half y w sons, whereas a sister ♀, also white, produced only white sons. In the offspring of 1036 (table 128), likewise, one ♀ among 69 which latter must have been ½ +/+, ½ +/y w, was phenotypically white and scalloped (no. 1195). Unfortunately, she was sterile. We did not succeed in isolating the translocation, which thus was lost. Some more data on this case will be found in the section on mutation (p. 512). But it is remarkable that in F_3 so many soft and spread individuals appeared, actually poi s, and that, in addition, F_2 (table 127) contained individuals with short bristles (marked bb), dwarfs, a notched male, and one soft blistered female. These types all failed to transmit their character to the offspring, and the soft blistered female was sterile. Obviously, together with the y suppression there had appeared by mutation poi s and, once, bran, as well as other types which might have been duplication effects in connection with the entire change. In the absence of other markers and criteria the analysis could not be pushed further.

m. poi AND bran ALLELES IN px bl

We saw that the most frequent mutants produced from px bl are the svr^{poi} alleles and the bran alleles, both of which appeared not only with the major upheavals in the stock affecting all px bl characters, but also individually on different occasions.

This necessitates a search for these mutants in the stock, maybe in heterozygous balanced condition. As a matter of fact, the stock was tested in the course of many years in all kinds of outcrosses which ought eventually to have revealed the presence of these mutants. But only poi s was ever found in the stock, though poi and bran alleles appeared repeatedly as new mutants. In some of the tables such occurrences were reported; others have not been mentioned. Thus, in a series of 17 backcrosses (px bl × triple) × triple, with 1,406 ♂♂, once 2 among 77 ♂, and another time 2 among 65 were pointed (svr^{poi}). Similar cases were found so frequently that the pointed mutants were not tested except in the cases already reported in the section on pointed. The same applies to the rarer occurrence of bran and their combination types, some of which have been described.

At one time only, namely, in the winter of 1937–38, had the mutant allele $svr^{poi\ s}$ spread in the stock and been frequently observed in crosses. Later, as has already been mentioned, very extensive special tests for poi and bran were made at different times with hundreds of individuals picked at random, and the results were always entirely negative. All the facts tend to show that px bl does not contain mutants as such at those loci, but that these mutants are rather frequently produced, may spread in the stock, and may disappear again.

n. THE SALIVARY-GLAND CHROMOSOMES OF px bl

Table 129 contains a check upon the salivary chromosomes of px bl made in the same way as for poi (see explanation, p. 345). An additional column contains a further check using 13 mass cultures with more than one gland per slide (one slide each). We see at once that the majority of the small rearrangements are the same as in pointed (see the discussion of poi and poi h). Ten additional changes have been noted. Plate 24, figure 1, shows a small deficiency of probably 3 bands in the X chromosome near the silver region, which was encountered only once. Plate 25, figure 3 shows another deficiency near the tip of X between the pn and w loci, which was encountered repeatedly. A little farther to the right another deficiency was found (pl. 24, fig. 2), which, according to the Bridges map, would be just to the left of ec. As an ec deficiency was found genetically, this was suspected to be its location. But Demeree localizes ec in 3 F1, 2. A test was excluded by the complete sterility of ec-deficient females, which can be distinguished only in the compound. In only one cross was the one-band deficiency no. 8 (pl. 25, fig. 8) found. This is exactly where vermilion is supposed to be located, and actually what might have been a v deficiency or a Dubinin effect involving v had been found.

In the second chromosome we have another of the tip deficiencies (no. 9), which have been sufficiently discussed for the pointed case. Near the right end of 2R the same disturbances in the a px region as were described for poi are frequently encountered. In addition, a frequent occurrence is Df. no. 13, which is located just to the right of the assumed loci for bs and ba (pl. 24, fig. 8). Another single-band deficiency at (2L) 26 Cl is not contained in the table, as not found in this series. It is located at or near the dp locus.

A transposition in 3L and a deficiency near by have been listed with an interrogation mark because no sufficiently clear picture could be established, though there is no doubt that something is abnormal at these loci. The former is the D region; the latter is to the right of h. The only rather conspicuous rearrangement found

at all is no. 20, and it occurred only once (pl. 26, fig. 5). It is a nonreciprocal translocation from (3R)86D1–E11, i.e., a region near Stubble to (3L)62, i.e., near ve. This largest translocation of about seven bands is of importance because it suggests

TABLE 129

SALIVARIES OF px bl

(Number of bottles: px bl × Ore, 11; Ore × px bl, 5; px bl homo, 6. Number of slides, 110.)

No.	Rearrangement	Number of slides positive			Check 13 outside heterozygous slides, mass	Plate and fig.	Found in n crosses out of 35
		px bl × Ore (55 slides)	Ore × px bl (25 slides)	px bl (30 slides)			
1	Df2T(X)1A 1–4[a]...	10 ♀	12 ♀	...	1	....	Twice all slides of cross in 10 crosses
2	Df(X)1C 1–3.....	...	....	...	1	24/1	
3	Df(X)3A2.....	1 (1) ♀ [b]	(2) ♀	...	1	25/3	In 5 crosses
4	T(X)3C[a].....	5	....	4 (2) ♀ [b]	..	25/2	Once all ♀ slides in 6 crosses
5	Df(X)3D 1–4.....	2 ♀	....	1 ♀	2	24/2	In 5 crosses
6	Df(X)4C9 and 4D1[a]	...	....	...	7	25/4	In 7 crosses
7	Df(X)9A2, 3[a].....	4 ♀	2 ♀	...	..	25/1, 2	In 5 crosses
8	Df(X)9F 13.....	2 ♀	....	...	..	25/8	Only in 1 cross
9	Df(2L)21A.....	7 ♀ ♂	1 ♀	1 ♀	..	....	In 4 crosses
10	T(2L)24AB[a].....	7 ♀ ♂	2 ♀ ♂	5 ♀ ♂	..	24/4	In 7 crosses
11	Df(2R)58D 5[a].....	...	....	6 ♀ ♂	..	26/1	In 4 crosses
12	Df(2R)58E[a].....	21 ♀ ♂	6 ♀ ♂	1 ♂	2	24/7	In 13 crosses, twice all slides
13	Df(2R)60D 5, 6.....	11 ♀ ♂	....	3 ♀ ♂	5	24/8	In 13 crosses
14	Df(2R)60F 4, 5[a]....	22 ♀ ♂	6 ♀ ♂	...	2	27/4	In 13 crosses, once all slides
15	T(3L)61A[a].....	7 ♀ ♂	1 ♀	...	1	....	In 4 crosses
16	Df(3L)61C 8[a].....	3 ♀ ♂	....	6 ♀	2	26/2	In 8 crosses
17	Tp?(3L)70BC, 71BC	12 ♀ ♂	6 ♀ ♂	1 ♀	2	....	In 11 crosses, once in all slides
18	Df(3L)67D?.....	...	3 ♀	...	..	....	In 1 cross only
19	Df(3R)84D 6, 7[a]....	16 ♀ ♂	6 ♀ ♂	25 ♀ ♂	..	26/4	In 15 crosses In 3 px bl and 1 Ore × px bl, all slides
20	T3R–3L.....	...	....	...	1	26/5	
21	Df(3R)86C 6–8[a]....	16 ♀ ♂	6 ♀ ♂	23 ♀ ♂	..	26/7	In 15 crosses In 3 px bl, 1 heterozygous, all slides
22	T(3R)100F[a].....	15 ♀ ♂	....	...	2	....	In 7 crosses
23	T(4)102F.....	3 ♀ ♂	1 ♀	6 ♀	..	27/1	In 7 crosses

[a] Found also in poi; see tables 45, 46.
[b] No. in parentheses probable, not certain cases.
♀♂ found both in female and male larvae.

clearly that the smaller deficiencies encountered are also actually deficiencies by translocation to another place, which, as a rule, could not be found (if not, some of the apparent small deficiencies are actually insertions). When one or two bands in a little-explored region or in a region of faint bands are disturbed, a decision between deficiency and insertion is difficult in the absence of interchromosomal attraction for such small sections, or their breaking in the process of preparation.

Finally, in a number of cases a thick conspicuous band was found attached to the tip of the fourth chromosome (no. 23, pl. 27, fig. 1). Its meaning is obscure. One other, more frequent, occurrence is not contained in the table because of analytical difficulties. It looks like a 3-band deficiency just at the chromocenter of 2R, where analysis is rather unreliable. We spent much time analyzing what probably is the plexus locus within the bulb in 58E of the second chromosome. Here there is always an abnormality. But the paleness of the bands did not permit an unequivocal interpretation. In plate 28, figures 1–4, a few drawings are given, one of them from a homozygote which might be interpreted as a 1-band deficiency or a 1-band duplication. As this structure is always found, the px in px bl seems to be based upon a small rearrangement.

It is of interest to know how many simultaneous individual rearrangements could be found in the slides taken from the offspring of one-pair matings. Table 130 con-

TABLE 130

NUMBER OF REARRANGEMENTS FOUND IN ONE-PAIR MATINGS

Class	No. crosses	Total no. rearrangements checked	Slides per cross	Maximum one cross	Minimum one cross	Average
px bl.....	22	23	5	10	1	5.9
svr^{poi}.....	8	16	5	10	5	7.4
$svr^{poi\,h}$.....	12	16	10	8	2	5.3

tains these counts, but it must be emphasized that the statistical picture is burdened with considerable errors because the counts relate to crosses in both directions and also to homozygous larvae. In the former case, the male cannot introduce some of the sex-linked deficiencies; in the latter, only heterozygous effects had been checked.

3. FURTHER FACTS ON MUTATION AT THE MAIN LOCI

a. THE STARTING POINT

The following general features of mutation in the px bl stock and its derivatives have been described:

1. The mutational phenomena occurred only once in a controlled-pair culture so that the entire offspring was affected. In this case, homozygous px and bs reverted to normal in one second chromosome. Simultaneously, heterozygous rudimentary (r) ♀ and one ♂ appeared; furthermore, svr^{poi} and probably also bran, which, however, was discovered only in a later generation. In addition, the plus modifiers for px changed.

2. Exactly the same happened later in a stock bottle, though the seriation was unknown. Again, px and bs reverted to +, svr^{poi} and bran appeared, but no rudimentary. In both cases also, other bran and svr alleles appeared (see nos. 1, 10 in table 151).

3. Afterward, the same mutants and alleles and reversions occurred occasionally either alone or in conjunction (see table 151). Thus bran and poi appeared repeatedly alone or together in inbred px bl or poi stocks or after outcrossing. Blistered reverted to plus with or without plexus; plexus reappeared where it had been absent; also svr^{poi} reverted to plus.

4. A series of alleles of svr^{po1} and bran appeared after the manner of mutants. Both these mutants and reversions tended to appear after outcrossing. This applies also to other mutants to be analzed below.

5. Px bl as well as pointed stocks were proved genetically to contain a number of small translocations and transpositions not including known loci.

6. Some of these could be found in the salivary chromosomes, others not. They contained only 1–3 bands.

7. Both stocks contained in the salivary chromosomes numerous small translocations and deficiencies which could not be proved genetically, since they probably did not contain known loci, the only exception being ec–Df.

8. A stock of the $svr^{po1\ h}$ allele of completely independent origin contained also a number of the same small rearrangements found in px bl and svr^{po1}.

9. The main mutants involved in the present discussion, px, bs, svr, and bran, cannot be called clear rearrangements; but all are associated sometimes or always with very small chromosomal changes in the respective regions.

We must now look into some of the details. If the hypothesis were proved that mutation is a chemical change produced in a gene molecule by chance or by unknown causes, all the facts would be side issues of no importance for the problem of mutation. We could be content to state that the px bl stock and its derivatives have a tendency to mutation and return mutation at the named loci, and the presentation of details beyond this statement would be surperflous. But the facts described, beginning with the change of an entire offspring of one pair from a closely inbred line which had been carefully watched, suggested that mutation is not a chance phenomenon localized in a gene molecule, but a phenomenon dependent upon conditions in the chromosomes themselves and somehow connected with minute rearrangements, though not necessarily being themselves visible rearrangements. Therefore all available details concerning the origin of the mutants may be of importance.

b. ADDITIONAL DETAILS OF THE FIRST CASE

I. General statement.—We begin with the original case which started this work, the details of which have been reported in the Introduction (see data and tables pp. 293 ff.). We found:

1. From a pair of inbred px bl, the ancestors of which had always bred in the manner described as typical for the stock, only 10 individual offspring were obtained, the parents still being alive and nothing being wrong otherwise. All females were blistered. Semisterility or inviability with what looked like a selection for blistering was the first abnormal phenomenon.

2. None of the offspring of these pure px bl flies were like the parents. Among the females, 7/8 were wild type. These turned out to be: (*a*) part homozygous +, i.e., in regard to px, bs, and the X chromosome, and a true-breeding wild type could be established; (*b*) a part was heterozygous for px, which turned out to be ordinary plexus; (*c*) some were heterozygous for rudimentary (r) and a normal X chromosome; (*d*) some had svr^{po1} in one and r in the other X chromosome; (*e*) the X chromosome with r could simultaneously contain svr^{po1}, though it is not certain that this was not the result of crossing over; (*f*) rudimentary could simultaneously be px/+.

3. Wild-type males equaled one-half of the females in number.

4. Whereas px extracted from heterozygous px/+ bred true to ordinary px, i.e.,

without bs and blistering, the low-grade px-flies, which were ⅛ of the females and about ⅕ of the males, with equality of the sexes, bred like the original px bl stock and obviously had the same constitution, i.e., also contained bs^p and the condition for blistering in the first chromosome.

5. There was one rudimentary male.

Thus, ⅛ of the female offspring and ⅛ of the expected male offspring of pure px bl remained px bl. Seven-eighths of the daughters had lost bs, and had also lost px either in both second chromosomes (return mutation to +) or only in one of them. The locus px, freed of bs, was ordinary px. Simultaneously, both r and svr^{po1} had appeared by mutation in the X chromosomes, probably in connection with the lethality of half of the males of this group alone, the px group having normal sexes. The single r ♂ might have been a survivor of the male lethal group. The female heterozygosity for svr^{po1} and r in the presence of one ♂ r proves that these mutational steps must have already occurred in the grandparents and therefore were connected somehow with the lethality of most of the parental generation. We know that all these features recurred repeatedly, with the exception of the mutant rudimentary, which remained rare. We might thus say that the origin of rudimentary is not necessarily involved in the origin of pointed or the return mutations at the px and bs loci. Though the "mutations" and the ratios obtained clearly indicate some orderly event, it is difficult to reconstruct what had happened. But it is clear that the words "mutation and reverse mutation in a gene" do not have much meaning in such a case. The clear and orderly interrelation of the two mutational and the two return-mutational steps indicate that they are all the result of some major happening which I can only visualize as a simultaneous change of a mechanical nature in the chromosomes, like a pattern change of some kind, though it cannot be described as yet in terms of definite translocations, etc. If we look at known facts the only possible parallels are found among larger and easily verified translocations. When the Blond translocation originated, the phenotypes Bld, Bld(1)Df, and Bld(2)Df soon appeared together. In this case, a relatively large reciprocal translocation with incomplete lethal deficiency-duplication classes could be located from the breeding results. But a similar case involving minute parts of the chromosome, may be even below one salivary band, and thus allowing for homozygous viable duplications and deficiencies, not visible in the salivary slides, could hardly be proved genetically when no known loci are involved in the changes. It is this parallelism which led me to doubt that the conception of simple gene mutations could explain our case and all the consequent facts which fall in line, though in the present case it is impossible to tell in concrete terms what had happened.

II. Further analysis.—The further facts of this first case are in agreement with such conclusions, as will be seen in this more detailed study:

The normal and low plexus segregants.—We begin with a short report concerning wild type and standard px which were recovered in the case of "upheaval," as we might describe the happenings under scrutiny. As reported in the pedigrees (table 1), wild-type flies appeared in the first (and subsequent) upheaval in the px bl stock, namely, 136 ♀ 70 ♂ +, one-half of the males obviously being lethal. Three pairs of these flies gave (*a*) normal females and rudimentary males, (*b*) normal females and pointed and rudimentary males, and (*c*) 148 ♀ 70 ♂ +. Later generations bred from wild type either bred true or segregated into normals and pointed, or normals,

TABLE 131

ORIGIN AND FURTHER GENERATIONS DERIVED FROM LOW plexus OUT OF px bl

Generation	No.	Cross	+		poi		rud		low px		px bl		Remarks
			♀	♂	♀	♂	♀	♂	♀	♂	♀	♂	
P	4203 B	px bl.....	..	..	..	..	..	..	..	..	All	All	
F_1	4474 B	px bl × px bl.....	136	70	..	..	..	1	18	19	..	..	
F_2	4612 B	4474 + × +.....	151	..	..	65	..	55	..	..	..	..	1 ♀ one side rud. wing and leglike structure
F_2	4614 B	4474 px × px.....	..	..	..	..	..	..	..	..	All	All	Breeds true
F_3	4765 B	4612 + × +.....	199	..	..	67	..	49	2	..	..	..	
F_3	4764 B	4612 + × rud.....	77	..	..	43	29	34	25	15	..	..	px not poi
F_4	4977 B	4764 + × poi.....	73	35	45	19	..	41	43[a]	29	..	..	
F_4	4978 B	4765 + × rud.....	28	53	44[b]	13	71	70	2?	..	..	..	
F_4	4979 B	4765 + × +.....	48	46	42[c]	34	..	..	..	..	..	..	
F_4	4988 B	4764 px × px.....	..	..	..	..	..	24	71	42[d]	..	..	1 ♀ 3 ♂ px spread blist (see below)
F_5	5173 B	4977 px × px.....	..	..	4	..	..	14	132	33	..	..	3 ♀ px poi 9 ♂ soft spread px blist (see below)
F_5	5176 B	4988 px × px.....	..	..	..	..	..	..	All	All	..	..	Breeds true
F_6	5345 B	5173 px × px.....	..	..	..	..	..	..	155	135	..	6	3 ♂ soft spread px bl

[a] 6 ♀ blist
[b] 8 ♀ short bristles
[c] ½ ♀ short bristles
[d] 9 ♀ 7 ♂ px and poi

pointed, and rudimentary. But some of them also contained plexus, as was reported in the pedigree and is to be reported in detail below. However, the wild type, which bred true for many generations, later twice produced a few rudimentary males, as will be reported in the section on rudimentary. Otherwise it bred completely true and was finally discarded. Crossover tests had been made for all chromosomes of the wild-type flies. They showed completely normal behavior, normal reciprocal classes, and normal sex ratios. The crossover values were somewhat high, e.g., 28.2 instead of 17 for the interval facet–cut. To all purposes, this "reverted" mutant line was normal. Normal true-breeding flies were later produced again when the mass-mutation phenomenon was repeated in the stocks. It may be emphasized here that these normal flies had simultaneously lost px, the bs allele present in the px bl stock, and the conditions required for blistering.

As recorded in table 1, a low-grade plexus appeared together with +, poi, and r from px bl, as well as with the recovered typical px bl type in the first occurrence of mass mutation. Part of the pedigree of this low px line, which has bred true ever since, has already been given in table 1. More details (only those relating to low px) are contained in table 131 (which presents also a number of broods already reported with the origin of other types).

This table shows the following. Low px first appeared in about ⅛ of the females and in the same number of males, of which otherwise ½ were lethal. Thus the type is somehow released from px bl by a combination of an autosomal and a sex-linked condition, the latter being heterozygous for a male lethal condition in the mother, while all px males were free of this X chromosome. But the low-plexus individuals, when one pair was tested, produced a complete return to the px bl type, which bred true. From the normals in F_2 as well as from normal females and rudimentary males low px again segregated in F_3—in one case only 2 among 200, which looks as if release by crossing over were involved; in the other case, one-fourth of the not rudimentary females and males. Both parents, then, were heterozygous for this px. Whether it recombined with rudimentary was not checked (but judging from later work with rudimentary, which contains px, it did). In the presence of plexus no pointed was visible, though px and pointed were visibly combined in F_4 and F_5; but this was produced by a new allele, to be discussed later. From now on the low px bred true, though rudimentary was still present and a new type plexus spread soft blistered male was segregated (see below). A stock of the low px was established and bred true to type for many years (under the name Tpx). From the very beginning the sex ratios were most variable where the low px type was involved. In F_3 there were 131 ♀ 92 ♂; in F_4, 161 ♀ 124 ♂; in F_5, 75 ♀ 76 ♂; in F_6, 139 ♀ 56 ♂; in F_7, 155 ♀ 144 ♂.

The low px stock was crossed to different stocks containing standard px, producing 100 per cent px flies of very low grade, which bred true. We may therefore assume that here the original px from which px bl was derived had been restored, by removing whatever was responsible for the px bl type, i.e., bs^p, enhancers of plexation, and the locus for blistering in the X chromosome. When low px first appeared it was still partly heterozygous for poi, r, or both, as table 132 of outcrosses shows. The crosses 5669–5712B were made immediately after the px type had appeared, the others about ten generations later when px had been selected. The first crosses all show a very high sex ratio, ranging from 1.9 to 3.4. (One reciprocal cross,

5735, is normal.) This shows that at this moment the px ♀ contained X chromosomes which produced lethal combinations in sons. This condition was obviously present in both X chromosomes, as the crosses segregating poi and rud or + and rud show. Those with + and poi are not decisive because poi is sometimes not clear. Most probably, the lethal classes result from combinations of the X chromosome with autosomes, the mother having been heterozygous for the autosomal conditions. Obviously, translocations 1→autosome were involved of the type proven to be present in poi. The presence of soft spread males suggests that the allele $svr^{poi\ bl}$ was also present. But it was not extracted from these crosses (see below).

TABLE 132

OUTCROSSES OF low px SOON AFTER ITS ORIGIN

No.	Cross	+		poi ♂	rud ♂	n♀ : 1♂	
		♀	♂				
5669 B	low px × 5 ple....	82	38	6	..	1.9	Some ♂ spread 1 ♂ abnormal abdomen; Bd and spread
5715 B	low px × ey.....	78	26	4	..	2.6	
5716 B	low px × ey.....	69	..	14	12	2.7	
5736 B	low px × X ple....	80	16	..	12	2.8	
5735 B	X ple × low px....	80	72	..	..	1.1	
5712 B	low px × triple...	54	16	..	..	3.4	2 ♂ soft, 2 ♂ soft spread
7673 B	low px × a sp.....	53	55	..	..	0.9	
7674 B	low px × a sp.....	32	27	..	..	1.2	
7675 B	low px × a sp.....	82	61	..	..	1.3	
7676 B	low px × a sp.....	58	48	..	..	1.2	
7677 B	low px × a sp.....	41	29	..	..	1.4	

Actually, in the beginning, when pointed or rudimentary or both were still contained in this low px line all the features described for pointed X chromosomes were still present. The same tests for all the chromosomes were made as are described for pointed, but the results were the same: lethality of the X chromosome containing pointed in combinations with two foreign right ends of second chromosomes as well as the right half of the third, lethal crossover classes in the first pointing in addition to a transposition, modifiers for pointed, and abnormal sex ratios. In view of the complete parallelism no further data are presented, which would only duplicate those presented for pointed. After pointed and rudimentary had been selected out, the still abnormal sex ratios indicated that some of the special first chromosome conditions were still present. A standard translocation test (Patterson) gave completely normal results.

Broad round (bran).—In the offspring of the line under discussion the mutant bran also appeared and became visible in the fourth generation. It is not probable that it had been overlooked wherever poi was present, because the combination of both, called soft blistered, is too conspicuous. But it might have been overlooked in broods without poi. However, its first appearance does not favor such a view. If present before, it ought to have become visible in a simple Mendelian ratio, which it did not. The pedigree is shown in table 133.

TABLE 133

PEDIGREE OF THE FIRST bran

No.	Cross	px		px poi		r		px etc.[a]		+		poi	
		♀	♂	♀	♂	♀	♂	♀	♂	♀	♂	♀	♂
4612 B	4474² + × +	..	..	..	..	..	55	..	..	151	..	..	65
4764 B	4612² + × r	25	15	..	..	49	32	..	..	76	..	..	33
4977 B	4764² + × poi	43 (6 bl)	29	..	..	..	41	..	..	73	35	45	19
4988 B	4764² px × px	62	35	9	7	..	24	1	3	..	..	..	..
5173 B	4977² px × px	129	33	4	..	..	14	..	9	..	..	..	..
5345 B	5173² px × px	155	141	..	..	..	..	..	3	..	..	..	..
5178 B	4988² px poi × px etc.[a]	37	12	..	..	..	10	57	27	..	..	..	..
5348 B	5178² px bran × px Mass	5 bran 195 37 bl	194 12 bl	..	..	..	16	3	3	..	..	..	..
5350 B	5178² px × px	36 20 bl	33 8 bl	.. ..	.. ..	.. ..	.. ..	.. ..	10	..	..	..	..
5351 B	5178² px etc. × px etc	10?	12?	..	..	..	..	47	56	..	..	..	..
5349 B	5178² px bran × px etc	141	135	..	..	..	..	43	49	..	..	..	..
5352 B	5178² px etc. × +	10	6	..	..	13	14	34	44	..	..	..	..
5345 B	5173² px × px Mass	155	135	..	..	..	..	..	9	..	..	..	..
5346 B	5173² px × px etc. Mass	165	171	23	8	..	..	14	10	..	..	..	..

[a] 2 px etc. = type plexus soft spread blistered = px bran/px bran, SVR$^{poi\ bl}$.

The first two generations contained neither bran nor any of the bran poi combinations. But in the third generation bred from px parents (4988) it turned out that the parents had been heterozygous for bran = 6/7 of the females (probably 7/8) were px, and so were half of the males. Two-thirds of the other males were rudimentary. Furthermore, there were 9 ♀ 7 ♂ px poi, i.e., px flies which clearly showed pointed wings, which ordinarily is not the case when px is combined with svr^{poi}. Actually, in this case a new poi allele had originated (see below). In addition, 1 ♀ 3 ♂♂ of a new type appeared with wings soft-textured, plexus, blistered, and spread (held at right angles to the body). We reported that this type turned out to be the combination of pointed blistered with plexus. Poi blist (see p. 356) is the combination of bran/bran with the allele $svr^{poi\ bl}$. The svr allele alone produces a wing which usually looks like pointed but is frequently soft-textured, with a tendency to spreading. In the presence of bran the poi blist phenotype is seen, pointed but blistered wings with a fluctuation toward pointed and singed. The additional presence of px makes for the new type just described, soft spr px bl. Thus the few individuals homozygous for px bran in the second chromosome and the allele $svr^{poi\ bl}$ in the first might be taken to indicate that bran had been present in some gametes of the px parents that one X chromosome of the mother had contained r (together with svr^{poi}) and the other had contained in the majority of the gametes either $+^{svr}$ or svr^{poi}, which latter does not show clearly with px. The presence of svr^{poi} is improbable because there were no soft blistered males and therefore the second X was $+^{svr}$. But in some of the gametes of both parents there must have arisen the allele $svr^{poi\ bl}$. Actually, the individuals registered as px poi also contained the poi bl allele and were heterozygous for bran. Thus about 1/8 of the segregants contained poi bl and most of them were heterozygous, with a few homozygous for bran.

From the same F_2 (4764) a pair + × poi were bred (4977). Here +, poi, and px segregated with a sex ratio near 2 : 1, and in addition as many r ♂♂ as poi ♀♀. If part of the px individuals were invisibly poi, the segregation would be in half females +, half poi, i.e., the mother had been poi/r. The insufficient number of r males is frequently found and is based upon lower viability. In this case the properly computed sex ratio is normal. No homozygous bran is present. But a subsequent generation from px parents (5173) segregated px and r males with a majority of females px (px ♀ not containing poi, as the next generation shows). In addition, 4 females px poi appear, i.e., px/px (bran/+?); $svr^{poi\ bl}$, and 9 ♂♂ soft spr px bl marked in the table "px etc.," i.e., px bran/px bran; $svr^{poi\ bl}$. Half of the females in the px and r classes are missing, which requires a lethal combination 1→autosome. Again, bran and the poi allele have made their appearance in what hardly looks like Mendelian ratios. A further generation bred from px flies (5345) contains 3 px etc. males among 144, i.e., again mutant-like appearance of bran and $svr^{poi\ bl}$.

The only px etc. female thus far obtained was sterile, but a female px poi from 4988 could be mated to a px etc. male. About 1/2 of the daughters were px etc., the others px; half the males were lethal, the rest about 1/2 px etc., 1/8 r, 1/4 px. Aside from the males, this shows, as already assumed, that the mother px poi had been bran/+; $svr^{poi\ bl}/svr^{poi\ bl}$, r, and that the px etc. father was bran/bran; $svr^{poi\ bl}$.

In this brood (5178) were found, in addition, 5 ♀ px and bran. Their offspring (5348, 5349) showed that they had been only heterozygous for bran, i.e., bran had been dominant in these flies. As this locus did not continue to breed as a dominant,

we must assume that dominance modifiers had been present. But we remember from the section on poi bl that dominant alleles of bran had twice been segregated from this stock, so that the possibility cannot be denied that the bran found here was not the ordinary bran which was isolated later. However, here px was still associated with the near-by bran. We shall return later to this dominance phenomenon, as well as to the combination of px with bran.

The type px etc. bred true except for a small number of individuals which looked like plexus. But a stock which was established soon died out. We shall return later to the fact that px together with bran always produced unviability and sterility. The other crosses in table 133 agree with the foregoing analysis. In this case, then, bran had appeared as a mutant, not in conjunction with the already present svr^{poi}, but only with the new allele $svr^{poi\ bl}$. We shall find that same association again.

At the time of these happenings a number of checks were made in order to throw light upon the first appearance of the combination of the two new mutants. Standard translocation checks were made. These were completely negative, showing that px etc., did not produce lethal hyper- or hypoploid combinations, not even clearly sublethal ones. The salivary chromosomes were checked, at that time only for translocations of a size easily discovered, such as Bld. The result was negative. First and second chromosomes of comparable phenotypes were both checked for deficiencies in the regions involved. The result was again negative. We also tried to establish a stock over y. F_1 showed normal ♀♀ and ♂♂ with soft, somewhat spread, wings which were found later to be typical of the poi bl allele. In F_2, bran segregated in the females and px, etc., in the males, and breeding from y, px bran/px bran × px etc. ♂♂ a stock was established which likewise died out after two generations.

When we tested the X chromosome in the backcross (px etc. × xple) × xple, no px etc. males were obtained as expected (no bran/bran). Otherwise the cross showed clearly the presence of a transposition from the left end to the right end of the first chromosome of the same type as was described above for poi. Plus and xple classes had normal sex ratios. All crossover classes with the right end present but the left end up to vermilion replaced were normal. But the classes containing the sc–ec region from the px etc. chromosome but with the right end replaced had extremely high sex ratios in favor of the females. For single crossovers the numbers of reciprocal classes of these categories were 39 ♀ 35 ♂ against 41 ♀ 9 ♂ (which is highly significant statistically). If both the left and the right ends are replaced, or only the intermediate part, sex ratios are normal. We do not know whether this transposition is in any way connected with the appearance of the two mutants.

A check of the second chromosome, also made immediately after the appearance of the mutants, showed a disturbance in the arc region (where bran is located). This results in sublethality of males in which the arc region from px etc. is replaced, i.e., a/a crossover males which still have the left part of the original second chromosome including the vg region. Thus all crossover classes which have in one second chromosome both the vg and a region from px etc. are normal, as are those in which both regions are replaced. But when the vg region from px etc. is present and the a region is replaced (even if the sp end is present), very few males survive. The numbers for the first group were 21 ♀ 32 ♂; the second group, 35 ♀ 6 ♂ (statistically highly significant). All 6 ♂ of the latter group are in the a sp class, none in the double crossover a class without sp, which puts the disturbance to the left of arc.

Unfortunately, circumstances forced me to break off at this point and prevented me from determining more closely what happened to this region.

Return mutation of plexus.—Once more, again only a few generations after the first upheaval, the type px etc. = bran px, $svr^{poi\ bl}$ homozygous was segregated in connection with happenings at the px locus, this time not reverse mutation to normal, but the reappearance of the lost mutant px. This remarkable case happened in the following way. The two alleles svr^{poi} and $svr^{poi\ h}$, both from inbred stock but completely independent in origin (see p. 299), were frequently crossed and gave a pointed compound. But once, strangely enough, plexus flies appeared in some F_2 and backcrosses. Poi was derived from px bl but never had shown any plexation.

TABLE 134

ORIGIN OF PX FROM poi × poi h

No.	Cross	pointed		px		px bl		Remarks
		♀	♂	♀	♂	♀	♂	
5833 B	(poi × poi h)² 5681².....	44	33	13	14	1	..	
5834 B	(poi × poi h)² 5681².....	73	79	23	16	1	..	
5877 B	(poi h × poi)² 5743².....	All	All	..	..	..	..	
5878 B	(poi h × poi)² 5743².....	All	All	..	..	..	..	
5839 B	(poi × poi h) 5681 × poi.	50	24	2	1	..	..	
5840 B	(poi × poi h 5681) × poi h	77	45	..	..	..	..	
5887–88 B	poi h × (poi h × poi) 5743	186	142	..	..	..	..	
5891 B	poi × (poi h × poi) 5743.	40	35	..	..	..	..	1 ♀ 4 ♂ soft blist spread poi not px
5889 B	(poi h × poi) 5743 × poi h	128	77	..	..	..	..	
5890 B	(poi h × poi) 5743 × poi.	79	65	..	..	..	..	

It had been bred under control for three generations of brother-sister matings, and afterward in stock bottles. Stocks were controlled and no px fly was ever found, nor an extra vein of the type indicative of heterozygous plexus. The same applies to pointed h, which had bred true for many more generations and was originally not derived from px. But in later years, i.e., more than five years after the crosses to be reported were made, one or two plexus flies occasionally were found in svr^{poi} bottles, certainly not more than one in thousands (breeding true as px after crossing to standard px). In innumerable one-pair crosses or in F_2 of outcrosses with poi a px fly was never found; this includes one very large series of poi × poi h and F_2 made just for this purpose. Table 134 contains all the F_2 results of 1935 in which px reappeared. Plexus flies appeared in two F_2 with poi mothers both derived from the same grandmother, and a few in a backcross of the same F_1 to a poi male, again from the same grandmother. None of the other combinations contained px flies, but one backcross of a male, again from the normal reciprocal F_1 no. 5743, to a poi female produced soft blistered spread flies, which, as we shall see, at once were producers of px flies, i.e., heterozygous px. (We recall that px does not clearly show pointed, and also that the pale body color is not reliable. This applies to the alleles poi and poi h, not to poi bl and poi si and others which are clearly visible with px. Later tests of the extracted px confirmed the absence of pointed.)

The sex ratios are remarkable. They are normal in the F_2 producing plexus, but not normal in the backcrosses, except the one with the soft blistered spread flies: twice the ratio nears 2 : 1 (257 ♀ : 147 ♂), twice it nears 4 : 3, namely, 264 ♀ : 207 ♂. The F_2 containing px flies has 229 pointed : 68 px, which is near a 3 : 1 ratio, though neither of the grandparents had shown plexus and none of their ancestors for many generations, including brother-sister matings over more generations. Nevertheless, the cross showed that one of the grandparents had contained plexus in a heterozygous condition.

The first idea to suggest itself is that the poi female, mother of F_1 no. 5681, carried simply heterozygous px from the ancestral px bl line. This can easily be disproved:

1. When the poi stock was established, it was first carried for some generations in brother-sister matings, later in mass culture. Segregating flies would have been noted, though it cannot be denied that by chance all matings were +/+ × px/+.

2. If this explanation were true, one-half of the F_1 flies would have been px/+, one-half +/+. Three F_2 and RF_2 which could show such heterozygosity all contained px. (This would not be a proof in itself.) But there was never an indication of the heterozygous px effect, for which the flies were closely watched and which otherwise was never absent.

3. The backcross 5839 which produced a few px flies could do this easily if a few sperm cells of the father from poi stock contained px.

4. We have met with other cases of unexpected reappearance of px in a few individuals, where a simple former heterozygosity is excluded. We cannot, however, exclude the presence of a px duplication in pointed, though it was never found in the many test crosses with second chromosome markers containing px.

5. Numerous crosses for the analysis of the pointed alleles were made simultaneously, but no px segregation occurred; the heterozygous px effect was never observed.

6. Unequivocal proof that something else had happened is the absence of pointed from part of the extracted plexus flies, though both parents had been homozygous pointed (or simplex). Details will be given at once. A stock which was established from selected plexus flies was free from poi.

7. There is the cross 5891 with a father from 5743, which latter did not produce px in whatever crosses. With a poi mother a few soft spread blistered flies (not px!) were produced which turned out to be heterozygous for px and homozygous for poi bl. It follows that px is either a return mutation occurring more or less regularly in poi, or that it is carried in a heterozygous condition covered by a closely linked duplication which only rarely is set free by crossing over. Thus it might or might not be relevant that px was set free after crossing the two poi alleles. But it is certainly important that svr^{poi} had simultaneously mutated back to +, i.e., reversed the original happenings, and that now bran and poi made their appearance.

Table 135 shows the F_3 results of breeding from the F_2 5834 and the backcross 5891. (In addition, the soft spread blistered males and px females and males were tested for deficiencies in the first and second chromosomes, without results.) The first two items of this table show a remarkable result. The plexus flies bred true to a plexus just as extreme as in the px bl stock, and furthermore, half of them, both males and females, were blistered; but half of the blistered males were missing, which is the case in both crosses. (In the standard px stock, blistered males are very

rare, within a normal sex ratio.) Thus we find the male lethal class, so frequent in outcrosses with poi, and simultaneously the new appearance of blistering in both sexes, male lethality being confined to the blistered class (106 ♀ px 111 ♀ px bl, 87 ♂ px 46 ♂ px bl), a condition which we already know to be typical for bs^{pp} in conjunction with px bl. As pointed certainly did not contain bs, which was tested innumerable times and could not have been overlooked, this means that bs had reappeared in the form of the allele bs^{pp} together with near-by px.

A further generation bred from not blistered flies gave 70 ♀ 35 ♂ all extreme plexus and blistered, one-half of the males missing, as was previously the case with px bl males (table 135). A line was extracted which has ever since bred true for strong plexus but varies in regard to blistering. A test made after five years showed only a few blistered flies, but after selecting had been done for some time most flies

TABLE 135

SOME F_3 FROM F_2 IN TABLE 134

No.	Parents	px		px bl		poi		soft px ± blist ± spread		poi blist	
		♀	♂	♀	♂	♀	♂	♀	♂	♀	♂
6046 B	5834 px	73	64	58	26	..	..	..	..	..	..
6047 B	5834 ♀ px bl ♂ px	33	23	53	20	..	..	..	..	..	..
6048 B	5834 pointed	..	..	..	..	73	39	..	..	..	..
6063 B	5891 ♀♂ soft spread bl	..	2	..	..	49	48	16	12	5	2

were blistered. We know from an earlier section that the allele bs^{pp} was present, which produces blistering in both sexes and high plexation, and this constitution was confirmed in the present case.

To return to the other crosses of table 135, we see that the pointed flies from the same F_2 5834 bred true to pointed. One count, however, showed ½ of the males missing, a sex-linked lethal obviously introduced from the grandparents. The strangest result was obtained from breeding the soft spread blistered individuals (not px) segregated from backcross 5891. About three-fourths of the offspring were pointed. The rest consisted of a majority of soft blistered plexus and partly spread individuals, indicating the presence of bran and poi bl; some females and males were pointed blistered without px; and two males were only plexus. Both parents had been heterozygous for px and homozygous for a poi allele (poi bl), px having been absent in two former generations. In this case bran had again obviously been somewhat dominant, as the blistering indicates, the other characters being produced by the poi allele. Bran and px, then, had arisen in the same second chromosome. (The 2 px ♂♂ were minus variants of the same class.) Also, there were 5 ♀ 7 ♂ pointed blistered. They turned out to be heterozygous for px and homozygous for bran and $svr^{poi\ bl}$; actually, the stock poi blist was derived from these individuals after segregating out px. As the parents had been bran px/+, $svr^{poi\ bl}$, the production of poi blist = bran px/bran, $svr^{poi\ bl}$ required either crossing over bran–px, which is not probable with so high a percentage, or a loss of px. Unfortunately, the 2 males px were not tested for bran, since at that time the constitution of poi bl had not yet been cleared up.

Thus we see in this line (1) the reappearance of px after crossing the two poi alleles, one of which was derived from px bl; (2) the reappearance of bs as bs^{pp}; (3) the mutation to bran; (4) the mutation to $svr^{poi\ bl}$ from the svr^{poi}; (5) the reversal of svr^{poi} to normal; (6) male lethal classes involving translocations and apparent transpositions within both first and second chromosomes, which might have been present already and need not necessarily have been involved in the happenings. It might be added that the new pointed blistered was immediately checked for translocations with the Patterson test, with negative results except for the already reported suppression of eyeless. The same negative results were obtained for px bs^{pp} which had arisen here.

A new feature of these happenings (no. 5) already mentioned was the disappearance of poi in part of the px flies. This first became apparent (px with ordinary poi

TABLE 136

F_1 Crosses of New px bl (See Table 135)

No.	Cross	♀ hetero-px	a ?	♂ poi	♂ px bl	+	poi blist	Remarks
6186 B	6046 px bl × b pr vg a sp	109	..	27	1	..	..	px hetero effect more pronounced than usual
6190 B	Reciprocal.....	24	3	..	..	21	..	
6212 B	6047 px bl × triple....	68	..	7	..	..	1	hetero-e^s effect
6231 B	6047 px bl × 5 ple.....	44	1	..	..	4	4	
6232 B	6047 px bl × X ple.....	137	30	40	..	..	1	
6210 B	6047^2 px.....	119	..	7	..	13	..	

and especially if blistered is difficult to recognize clearly) when the new px bl type (with bs^{pp}) was checked for crossover in different chromosomes immediately after its appearance. The F_1 crosses are contained in table 136. The mothers px or px bl twice produced both pointed and normal sons, the others only pointed sons. Six males were pointed blistered, i.e., bran + poi bl, again with some dominance of bran. This shows again the presence of the new bran and the allele $svr^{poi\ bl}$ in a few gametes of the new px bs^{pp} ♀. The heterozygous a and e effects occurred just as in the ancestral pointed line. The heterozygous plexus effect was more pronounced than usual, probably owing to the bs^{pp} allele. Most conspicuous are the sex ratios, both in the presence of only poi or of poi and + males. They were 3.9 : 1, 8.5 : 1, 5.6 : 1, 4 : 1, 6 : 1. Obviously, lethal recombinations of X chromosomes and autosomes are found, which means that the mother was heterozygous for translocations from X to autosomes producing male X-deficient classes. Again, we suspect that these lethal recombinations had some relation to the changes under discussion. (The stock which was selected from px bl gave normal sex ratios when tested after many generations. The absence of lethal classes in translocation tests must be explained as in former cases.) We cannot help assuming that the few poi blist and one px bl ♂ "mutant" were somehow survivors of otherwise missing classes.

Both males + and poi were tested in backcrosses; they were px/+, as expected, and otherwise gave normal results. The females, too, were tested for the second chromosome in quintuple backcrosses. They might have been poi/+ or +/+ for the X chromosome. Actually, there was no suppression of speck. Only 19 among 110 ♂

TABLE 137

OFFSPRING OF FLIES FROM THE CHANGED 369 STOCK

No.	Parents	+		poi		soft bl		px (bl)		px etc.[a]		poi sing		Remarks
		♀	♂	♀	♂	♀	♂	♀	♂	♀	♂	♀	♂	
3969	♀♂ poi sing.....	6	10	5	10	75	30	..	..	..	11	..	..	+ and poi hetero-px
3970	♀♂ +.....	..	..	9	19	22	6	3	4	..	1	..	..	poi not clear
4481	♀♂ +.....	44	54	..	..	..	..	13	22	..	9[b]	..	..	
4482	♀♂ +.....	50	38	12	18	.:	..	9	11	..	..	11	4	15 ♀ 11 ♂ px poi blist
4491	♀♂ +.....	64	54	20	19	..	..	15	5	..	3	21	3	Part + hetero-px
4492	♀♂ +.....	94	65	..	26	..	..	25	21	..	3	..	..	

[a] px etc. = type plexus soft spread blistered = px bran/px bran, SVR$^{poi\ bl}$.
[b] 8 without px. + ♂ poi ?

which could show it were registered as pointed, all in the normal class. The other abnormalities were: (1) In the noncrossover quintuple class ½ ♂ were missing (69 : 39). These might be the expected poi ♂. (2) In the large crossover classes containing the a locus, half of the ♂♂ were missing (88 ♀ : 40 ♂). (3) In the + class (with 19 ♂ registered as poi) the sex ratio was 107 : 74 = 1.4. If the missing males are added to the 19 poi ♂, ♂ equality of + and poi is seen (55 : 52). Thus it is possible that ⅔ poi ♂ were lethal in the + class, and all in the quintuple classes and those containing arc. The arc region is again involved, in this case being needed for survival of pointed. The complete sex ratio was 300 : 193 = 1.7. (Crossover values did not furnish further information, as was always the case in the present study, probably because only minute rearrangements were involved.) Thus, we see again a complicated relation of the arc region with the X chromosome.

c. THE SECOND UPHEAVAL

In the Introduction, we reported upon another "upheaval" in the px bl line which likewise resulted in the appearance of bran and poi alleles and their typical recombinations, together with the disappearance—so-called return mutation—of px and bs. The line in question had already been extracted for the bs^{pp} allele, which had appeared under the following circumstances. In a bottle of px bl, 1 ♀ 3 ♂ were found notched, otherwise typical px bl. The males were tested in F_1 and F_2 with y and notches did not appear again. One notched pair gave only 8 ♀ ♂ offspring, not notched but blistered. A subsequent generation contained only extremely plexus blistered individuals, females as well as males, and this new condition bred true, though not all individuals were blistered. The stock remained so for years and was kept as no. 369. It turned out that this was actually px bl with the higher allele bs^{pp} present (see p. 433). There was no more notching, but it might be more than a coincidence that notching appears in males with bran opposite an a px deficiency, which suggests that the beginning had, again, been something like a deficiency by translocation.

After three and one-half years in which nothing happened in this stock, one of the bottles again contained, in addition to the type of the stock, wild type, low plexus, pointed, pointed singed, and soft spread plexus blistered flies. Thus, not only had px and bs^{pp} disappeared again, but pointed or other alleles of svr^{po1} and also bran had appeared in a part of the flies. Table 137 gives the results of breeding from 5 pairs out of that bottle. The following is an attempt to analyze these happenings.

The parents were wild type four times. All turned out to be heterozygous for px, which segregated altogether as 56 ♀ 60 ♂ among 334 ♀ 312 ♂, i.e., a ratio of 4–5 : 1. Once (4481) the parents contained neither poi nor bran, and segregated px in nearly a 3 : 1 ratio, which means that no lethal or poorly stable combination with the second chromosome occurred. In this case a relatively large number of "px etc." males segregated, of which, however, only 1 was px, 8 being only soft blistered spread (but not of the "soft blistered" type containing poi with bran), i.e., they contained bran and poi blist. But there is a possibility that the mother was heterozygous for poi, since part of the males might have been poi with poor expressivity. In no. 3970, only 1 px etc. ♂ segregated among 30 ♂. Plexus segregated in a very high ratio. More than half ♀♀ and few ♂♂ were soft blistered. This normally requires that one of the parents be homozygous, the other heterozygous for bran, and both poi; neither of

which had been visibly the case. However, as the offspring did not permit clear distinction between + and poi, some of the modifiers of the phenotype might have been involved. But even then one of the parents ought to have been soft blist, not normal. In 4491 the ratio + : px is again very high, 7 : 1 for ♀♀ and 9 : 1 for ♂♂. About half of the females are pointed but only one-fourth of the males, the other fourth being missing; again, the father must have been poi without showing it, and the mother poi/+. We shall see in table 138 that the extracted pointed singed flies bred true. They were extracted simultaneously from a sister brood, 4482 (p. 484), and shown to contain the new alleles bran^{s} and svr$^{poi\ s1}$, which together produced the poi sing type (varying into poi), and in the presence of px the type plexus pointed blistered. Thus, at least the alleles bran, bran^{s}, poi bl, and poi si appeared after the return mutation of px and bs^{pp} in this stock, and eventually also poi.[13]

Still more complicated are the offspring of 3969, with both parents poi sing from the stock under scrutiny. It is impossible that this poi sing was the one just mentioned (bran^{s}+ poi si), which latter breeds true. Seven-eighths of the daughters were soft blistered, a result which is only possible if both parents have some compound of bran alleles and one is heterozygous for a compound of poi alleles one of which does give ordinary poi (+ flies being probably poi) with the one-fourth of the segregating homozygous bran allele. As bran^{s} has no visible action alone, nor with poi (only with poi si), the parents might have been bran^{s}/bran, which would segregate ¼ bran^{s}/bran^{s}. As ⅞ ♀ were soft blistered, bran/bran and bran^{s}/bran must give soft blistered with both possible poi compounds; but as the parents were soft blistered, these combinations for poi must not have existed in the parents. This is only possible if the mother had one poi compound and the father a different poi allele. As part of the sons (probably one-half, the other half being lost owing to the poor viability of the type) were of the type px etc., which contains bran and poi bl, the maternal compound could have been poi si/poi bl. Thus the cross had been

bran/bran^{s}, poi si/poi bl × bran/bran^{s}, poi ?

Six of eight recombinations have bran/bran or bran/bran^{s} with, in the daughters, either poi si/poi ? or poi bl/poi ?. As all are soft blistered, poi ? can be neither poi si nor poi bl (see table of phenotypes). One-fourth of the daughters are bran^{s}/bran^{s}, again with both poi combinations. As one is actually soft blist, the other poi (incl. plus), poi bl/poi ? obviously produced also soft blistered with bran^{s}, but poi si/poi ? only pointed. In the sons the results would agree with this interpretation, bran^{s}/bran^{s}; poi si being the ⅛ poi and plus sons, the rest being ½ soft blistered with bran/bran etc. and poi si and ½ (poorly viable) soft spread blist with poi bl. But there is one difficulty left: all poi blist soft spread males are plexus and no females px are found. The parents must have been px/+, and px/px appeared only in males—moreover, only in males with poi bl. This cannot be visualized. The only visible explanation is that only one of the parents was px/+ and that px was more dominant than usual in the presence of poi bl. As the stock originally contained bs^{pp}, which increases the heterozygous effect, this is rather probable. At the time of this experiment the different bran and poi alleles were just being isolated, so that the decisive tests could not be made. But a comparison with the simultaneous

[13] We add that a contamination is excluded because bran^{s}, poi si, and poi dish had not existed before, while bran was present in combination with near-by px. The same is true for bran^{4}. Furthermore, no pure bran stock was kept at that time.

analysis of the changed stock 369 shows that the alleles needed for the foregoing interpretation had actually been produced in this stock.

Still another complication was found which could only be understood after the different bran and poi alleles had been analyzed. When analyzing the poi sing types from 369 which were combinations of bran^s and poi si, bran^s alone having no visible effect, we found a low plexus poi sing male which had no pointed wings. It was crossed to Oregon, and in a mass F_2, normal, plexus, bran, and px bran females and males, and pointed and pointed singed males segregated. The original father thus had been heterozygous for plexus, which had shown more dominance than usual, but also for bran, which is located next to px, i.e., px bran/bran, and the mass F_2 permitted the combinations of px bran and bran homozygous, i.e., px bran/px bran, bran/bran, and px bran/bran. But there were also many px without bran, too many to be crossovers; furthermore, no soft blistered appeared. In addition, poi and poi sing males appeared in a number far below one-half (12 poi, 1 poi sing among 85 males). This looks as if poi si had appeared as a mutant in a part of the F_1 males, which would mean in one-fourth of the gametes with the X from the original father.

All segregants of this F_2 were tested. Bran inbred or crossed with a bran stock was sterile in four cases. Bran px was twice sterile among four bottles in mass culture; twice it bred true, but in small numbers. A stock was established but died out, showing that the sterility of soft blist px, discussed above, was due to the bran px combination, as was found before. Since we had found a one-band deficiency in what probably is the bran locus in at least one allele, and also a one-band deficiency at or near the px locus, this might furnish the explanation. Once, bran px from one F_2 was tested with bran stock. The F_1 was normal (not bran!) and segregated in the next generation into +, bran, px, and px bran, showing that the tested bran px ♂ had either been heterozygous bran px/px with considerable dominance of bran or homozygous for a bran allele, which does not give broad round together with bran. The same phenomenon was observed when + × bran px was bred from one F_2. It segregated into ½ + and ½ px, showing that + had been heterozygous for px. Moreover, all px flies showed transition from + to bran, including both extremes. The same was true in F_3 made from bran px × poi, in which poi proved to be also px/+. The F_2 ♂ poi singed was mated to a sister bran. The offspring of half bran, half normal showed this male to have been bran/+, whereas all other poi males which were tested did not contain bran. Thus poi had originated by mutation, as was already suspected, in gametes not containing bran, though px could be present. But in one gamete poi had originated in an F_1 mother heterozygous for bran. Actually the poi mutant reoccured in F_2: one pair + × bran produced 48 ♀ 31 ♂ + 2 ♂ poi!

It turned out that the poi which had appeared in this group was the allele svr$^{poi\ bl}$, since typical poi blist flies segregated in F_4 from bran px × + in F_3 (together with bran and bran px) and also from F_3 bran × bran out of bran × poi sing in F_2, as well as from normals of F_3 out of the same F_2. As poi blist flies tend to show a phenotypic variation from poi over poi sing to poi blist, the possibility exists that some of the poi flies of F_2 were actually poi blist, i.e., bran/bran, svr$^{poi\ bl}$. Tests, however, did not show them to be homozygous for bran, so that the former discussion of those poi males is not impaired except that the allele in question is poi bl, which is not always distinguishable in the absence of bran.

TABLE 138

EXTRACTION OF bs^{pp}, bran^{3}, AND poi si FROM THE 369 STOCK

No.	Cross	px extreme		px extreme blist		px poi blist		Remarks
		♀	♂	♀	♂	♀	♂	
4490	Extreme px bl from stock.....	50	48	25	22	..	..	
4662	4481^{2} px bl × px (see table 7)...	..	67	63	25	..	..	Extra hair and bristles; 1 ♀ 1 ♂ low px
4681	4490^{2} px bl.....	34	40	..	..	59	12	9 ♀ 9 ♂ px poi not blist; px poi are hairy
4682	4492^{2} + × px etc. (see table 7).	27	35	11	1	..	..	44 ♀ 53 ♂ +; px is not extreme; short bristles in all classes
4912 ff	4662^{2} diff. comb.....	..	Some	All	Most			Breeds true
4956	4681^{2} px, or px poi, or px poi bl.	..	..	..	..	All ±	All ±	Breeds true

TABLE 139

SELECTION IN STOCK px bl 369

No.		+		poi		px poi bl		px		poi sing		Remarks
		♀	♂	♀	♂	♀	♂	♀	♂	♀	♂	
4482 F_1	♀♂ + from stock	50	38	13	18	15	..	9	11	11	4	
4491 F_1	♀♂ + from stock	64	54	20	19	..	..	15	5	21	3	3 ♂ px etc.
4663 F_2	4482² poi sing	..	..	22	36	..	..	2	6	48	20	20 ♀ 11 ♂ px poi sing
4664 F_2	4482² poi sing	..	..	36	40	..	..	..	..	34	12	Extra venation
4665 F_2	4482² poi	..	..	30	36	..	..	3	28	57	7	30 ♀ 4 ♂ poi sing all px; px ♂ poi ?
4666 F_2	4482² poi	1	..	37	70	..	..	..	..	35	1	
4667 F_2	4482² +	81	40	..	13	..	..	..	..	..	13	
4668 F_2	4482² + × poi	29	34	11	25	..	..	11	14	11	9	5 ♀ 3 ♂ poi sing = px
4683 F_2	4491² poi sing	..	..	20	47	..	..	..	..	54	13	♀ hairy, 4 ♂ poi sing spread
4902 F_3	4664² poi sing	..	..	40	75	..	..	..	..	60	37	25 ♀ 28 ♂ poi sing all px stock
4903 F_3	4665² poi × px poi	..	..	33	45	..	..	..	..	72	84	39 ♀ 72 ♂ poi sing all px; part singed
4904 F_3	4665² poi	..	..	52	52	..	..	..	..	20	30	All poi sing px; male not sing
4905 F_3	4665² px poi sing	..	..	..	..	..	..	..	..	38	43	All px 9 ♀ 19 ♂ not sing
4906 F_3	4666² poi	..	..	40	66	..	..	..	..	26	14	
4908 F_3	4666² poi sing × poi	..	..	10	35	..	..	..	..	30	7	
4911 F_3	4667² + × poi sing	60	54	..	..	..	..	18	22	..	..	
4920 F_3	4663² poi sing	..	..	46	64	..	..	..	..	46	3	
4918 F_3	4663² poi px sing	..	..	..	..	..	..	All	All	..	..	All singed stock
4921 F_3	4663² poi sing × poi sing px	..	..	..	Part	..	..	..	..	All	Most	
4960 F_3	4683² poi sing	..	..	..	Part	..	..	..	..	All	Most	
4489 F_1	♀♂ px stock	..	..	..	..	25	1	54	75	..	..	px is poi
4679 F_2	4489² px poi bl	..	..	..	..	35	13	28	24	..	..	px is poi
4948 F_3	4679² px poi	..	..	..	..	Most	Few	Few	Most	..	..	♀ bb achi
4949 F_3	4679² px poi	..	..	..	..	Most	Few	Few	Most	..	..	No achi stock
4950 F_3	4679² px poi blist	..	..	..	..	Most	Most	Few	Few	..	..	
4951 F_3	4679² px poi blist	..	..	..	..	Few	Few	Most	Most	..	..	Few ♀ achi
5066–67 F_4	4948² achi ♀	..	..	..	..	Most	Most	Few	Few	..	..	Most ♀ bb achi
5160 F_5	5067² achi	..	..	..	..	Most	Most	Few	Few	..	..	Most ♀ bb achi stock

One more F_3 cross ought to be mentioned (no. 4619), another cross in which a heterozygous bran was mistaken for a homozygous one, both being heterozygous for px. The result was:

No. 4619 F^3 from bran × bran (?)
16 ♀ 20 ♂ bran
20 ♀ 11 ♂ bran px
44 ♀ 13 ♂ +
12 ♂ poi (soft)
1 ♀ px

The parents were clearly bran px/+, poi bl/+ × bran px/bran +, and the expectation was: ♀ ½ +, ¼ bran px, ¼ bran; ♂ ⅜ +, ⅜ poi, ⅛ bran, ⅛ bran px, ⅛ poi bl, ⅛ poi bl px. The females agree with the expectation. The sex ratio is 81 : 56 = 1.4, i.e., about ¼ of the males are missing. Clearly, poi bl and poi bl px are missing, and the + and poi classes are deficient, while too many bran males appear. A male lethal condition is present for the poi X together with homozygous second chromosomes carrying bran. The one px ♀ (fertilized when found) obviously was one of the rare crossovers bran–px fertilized by a bran px sperm.

Thus, mutation to poi bl in some of the F_1 female gametes explains part of the results. Furthermore, the original male must have been a compound of $bran^3$ with no visible expression and another bran allele, $bran^4$ which in homozygous condition has the phenotype bran, variable towards plus, and in compound with $bran^3$ is more or less intermediate; with poi bl it gives the poi blist type. The linkage of $bran^4$ with px, a combination which is rather unviable, made a further analysis impossible.

Tables 138 and 139 contain data on some of the broods of generations that followed those reported in table 137, in which further alleles became visible. Table 138 shows the extraction of px bl containing the allele bs^{pp} breeding true for an extreme px bl in both sexes but varying toward nonblistering, mostly in males. Also, there was a tendency to extra hair and bristles, which, however, later disappeared from the stock. The table shows that this condition could be found and selected in the changed stock (4490, 4681, 4958), but that the latter also contained a poi and a bran allele (at least) which produced pointed blistered and rather slender wings. These segregated in F_2 (4681) in what looks like a 1 : 2 ratio for females. Actually, this turned out again to be the combination $bran^3$ px/$bran^3$ px, poi si, which we had already found to be derived from low px in this stock. The extreme px bl type also had segregated from normals in the stock (4481, table 137) and again bred true (4662, 4912). (In 4662 one pair of low px appeared which did not reproduce; it could therefore not be ascertained whether a reversal of bs^{pp} had occurred.) Thus the bs allele bs^{pp} had remained from the original stock with or without the new pointed and bran alleles and in the presence of px. We know already that svr^{po^1} does not show clearly in the presence of px, but that poi bl does, and so does the new allele poi si, which then could not be present in the homo- or hemizygous condition before it became visible.

Partly the same, partly different happenings occurred in the related lines reported in table 139. From a normal pair (+, 4482) from the same stock (the px bl 369 stock with return mutation, etc.) half normals, half pointed were produced with a high sex ratio in the + and px classes; px segregated normally in the + females, and in too great numbers in the poi females; there were no px males in the

poi class. About one-fourth of the poi flies in both sexes were "singed," i.e., had a singed-looking spot near the anterior edge or the tip of the wing. The females with both px and poi were blistered. Obviously, the already described combination bran^s/bran^s, poi si with or without px had segregated. This means that one of the + parents had been heterozygous for bran^s and px in one second chromosome, and that the other parent had been bran^s/bran^s px (bran^s has no effect without poi si). Also, the mother must have been heterozygous and the father hemizygous for poi si. A similar regregation occurred in another F_1 from normal parents (4491). The table shows that the extracted pointed types with or without singed could be heterozygous for px, which segregated with the varying ratios already known. The combination px poi sing could be easily extracted as a true breeding stock, though a varying number of flies were not singed. (Actually, this is the origin of the bran^s; poi si combination described above, p. 386.) Pointed singed without px seemed to segregate into poi and pointed singed. But it turned out that both groups have the same genetic basis, the singed character being variable; the majority of females were usualy singed, as were the minority of males, with a considerable variation in individual broods. The stock with px poi singed later changed, so far as the singed spot became a regular blister. Another line of the same was extracted (see 4489) which from the beginning had blisters instead of singed spots. Both were genetically alike, as described. Also, px poi blist was extracted and turned out, as described, to be the same combination plus plexus and bs^{pp}.

One more characteristic poi allele was obtained from the same stock. A pair of px flies from the same 369 stock produced (4489, lower part of table 139) a majority of offspring of the type px poi, and a minority, almost all females, of the same type and blistered. The parents must have been homozygous for a poi allele without showing it, and it might be assumed that we had again the bran^s px, poi si combination, which would mean that the parents were heterozygous for bran^s. (The sexual difference could have been purely phenotypical.) The px poi blist flies reproduced their type in the next generation, though part of the flies were not blistered. Four F_3 were bred from blistered and not blistered flies. Two of them behaved as if they were the bran^s, poi si combination (see table 139). In one, most of the females had short bristles (phenotype bb) and poorly chitinized (etched) abdomen, as is found with higher bb alleles; both traits, however, also found with deficiencies in the a px region, a type called here "achitinous" (abbr.: achi). These flies were very pale, with little or disheveled hair and bristles on the abdominal tergites. In another brood only a few females had this character. Selection was made for the pale flies with and without achi. In some of the established stocks the achi character soon disappeared, showing that it was not simply due to a bb allele. But the pale etc. phenotype turned out to be a new allele, poi dish (see p. 390), which continued breeding true with px blist simultaneously visible. Tests showed the presence of a low bb allele with very little compound effect with bb. The achi type therefore had required something else, probably in the bran region, as discussed above. Also, the presence of bran^s was tested and proved.

The happenings in this pedigree are rather difficult to visualize. The original parents must have possessed poi si and bran^s heterozygous, arisen in the reverted px bl stock. The allele poi dish was most probably already present as a compound with poi si, but had been overlooked in the F_2 males, and segregated out in F_3. The

simultaneous appearance of the bb allele (or its becoming homozygous) may or may not have been a chance accident. Another parallel case (see p. 387) points to some relation between the two events, and the same is true for the appearance of the achi-enhancing condition, suspected to be located in the arc region, and analyzed in other similar cases (see p. 393).

Altogether, then, in the selected px bl stock containing bs^{pp} the return mutations from px and bs to + arose, and simultaneously the mutants bran, $bran^3$, $bran^4$, poi, poi si, poi bl, poi dish spread in the stock. Also, bb and something in the a region (the achi-enhancer) were involved. But the bran alleles originated in the second chromosome with px as well as in those with $+^{px}$, the small distance making an ex-

TABLE 140

STERILITY OF THE bran–px COMBINATION

Gen.	No.	Cross	low px		soft bl px		bran		Remarks
			♀	♂	♀	♂	♀	♂	
F_1	581	low px × low px.....	About 50	About 50	..	2	..	..	
F_2	719	581² px × soft bl px..	55	60	11	11	..	..	
F_3	962	719² soft bl px.....	..	..	6	7	..	..	
F_3	1015	719² px.....	129	7	..	1	..	..	♂ px-like hetero-px
F_4	1098	962² soft bl px mass.	..	..	12	5	..	..	No more offspring
F_4	1158	1015² px × hetero-px	..	..	5	7	42	39	Two others sterile
F_4	1159	1015² px × hetero-px	..	..	12	10[a]	49	56	

[a] 3 abn. abd.

change by crossover improbable. As in former cases, it is hardly possible to relate the events to each other in a simple diagrammatical way, though there can be no doubt that such an interrelation exists.

d. bran AND plexus AND IRREGULARITIES AT THE TIME OF MUTATION

There is another group of facts which must be considered relevant, though no detailed interpretation could be derived from it. We have discussed above the type soft blistered, which is genetically a combination of some bran and poi alleles and which was found whenever one of them appeared by mutation in the presence of the other or whenever both mutated simultaneously. Soft blistered has always been bred without difficulty, but when it originated while px was still present it was practically sterile, as already mentioned. Table 140 shows such a case. The F_1 parents were derived from one of the stock bottles of px bl I in which low px, px/+, and soft blist flies had appeared. The offspring of the first cross were all px as expected, and there were two soft blist px males, i.e., bran px/bran px. No bran was registered among the px class. But this might have been overlooked if it was present in only a few individuals. The px parents might have been heterozygous for bran and homozygous for px and the mother in addition heterozygous for poi, both just arisen in the stock. The expectation had been ¼ ♀♀ bran px, ⅛ ♂♂ bran px and ⅛ ♂♂ soft blist px, of which only 2 ♂♂ and maybe a few overlooked bran px ♀♂ survived. These soft blistered males were crossed to their sisters and F_2 segregated into px and soft blist px. This requires that the mother be heterozygous for both bran

and poi. The expectation is ¼ ♀ and ♂ soft px blist, ¼ ♀ ♂ bran px, ¼ ♀ ♂ px poi, ¼ ♀ ♂ px. Pointed (i.e., svr^{poi}) with px is not easily seen. No bran px were recorded, and otherwise the ratios were not perfect. Extracted soft blist px bred true, as expected, but were highly infertile. F_4 was bred from all 13 F_3 flies and only 17 F_4 flies were obtained, which latter did not reproduce at all. Thus bran with poi, just arisen in the presence of px, is almost sterile. The px flies of F_2 gave in F_3 only px daughters and px soft blist sons with a sex ratio of 15 : 1. This indicated male lethal recombinations of the first, and probably of the second and third autosomes, as was observed before when these mutants appeared. Simultaneously, the few males had lost px in one chromosome; their phenotype was that of px/+, and so was part of their offspring. This in F_4 consisted of about ⅝ bran and hetero-px ♀ and ♂, and ⅛

TABLE 141

SELECTION FROM CHANGED STOCK px bl I

Gen.	No.	Cross	+		low px		soft bl		bran		Remarks
			♀	♂	♀	♂	♀	♂	♀	♂	
F_1	579	+ × soft blist (stock).	57	54	..	..	..	..	..	..	Some ♀♂ + hetero-px type
F_1	580	+ × soft blist (stock).	35	31	7	13	..	..	..	..	Some ♀♂ + hetero-px type
F_2	715	579² ♀ hetero-px, ♂ +.	43	12	..	..	..	25	66	36	+ = hetero-px
F_2	716	579² ♀ hetero-px, ♂ +.	50	43	16	15	1	15	..	..	3 ♀ 3 ♂ px bl
F_2	717	579² +.....	..	..	..	..	2	35	61	40	
F_3	973	717² bran.....	..	..	..	..	..	..	All	All	
F_3	974	715 × 717 bran.....	..	..	..	..	..	..	All	All	Stock

soft blist, with a normal sex ratio. Two of the F_3 px/+ males were sterile. In both cases the two F_3 (1015) parents bred true to bran, which they had not shown, and they were heterozygous for pointed, which, however, appeared in F_3 only in ⅙ instead of ½ of the offspring. But bran had become clearly viable by becoming heterozygous for px! Bran was not further selected, since it had been isolated simultaneously from other crosses. This is to be regretted because thus we do not know which allele was present. A detailed interpretation is certainly difficult, but we see again relations between the happenings at the px, bran, and poi loci involving mutation and what looks like return mutation, with the simultaneous appearance of lethal male classes.

In the same px bl stock from which the low px of table 140 originated there appeared wild-type flies and soft blistered males. The latter turned out to be the bran-poi combination without plexus and completely viable. Table 141 shows that wild type and soft blistered could be heterozygous for px and that wild type did not contain pointed. Soft blistered is of course the bran-poi combination, but again a few additional complications were present in connection with the appearance of bran and poi and the loss of px and bs from the px bl stock. Table 141 shows the first generations.

In F_1 px segregated once, in which therefore soft blist had been heterozygous. F_2 579 showed that here also one of the parents had been heterozygous. We see that two of the F_2 segregated bran without px, which had been introduced by the soft

TABLE 142

ORIGIN OF bran WITH AND WITHOUT px

Gen.	No.	Cross	+ (poi?)		px		soft bl		soft bl px		Remarks
			♀	♂	♀	♂	♀	♂	♀	♂	
F_1	578	px × soft blist.....	15	13	..	..	7	14	..	..	+ = hetero-px
F_2	712	578² soft blist.....	7	5	3	3	26	29	6	6	1 ♀ soft blist is sooty
F_2	713	578² soft blist.....	..	3	3	1	36	40	19	17	1 ♀ 1 wing slender
F_2	714	578² soft blist.....	71	..	21	1	3	24	1	3	1 ♀ high px 1 ♀ px blist 2 + ♀ scute
F_3	999	713 × 715, soft bl.....	..	..	..	..	All	All			
F_3	1009	712² soft bl (♀ dp type)..	..	..	..	..	..	..	2	6	
F_3	1011	712² soft bl.....	..	..	..	..	..	..	3	3	4 more F_3 from soft bl px sterile
F_4	1150	999² soft bl.....	..	..	..	..	All	All	..	..	Normal fertility
F_4	1154	1009² soft bl.....	..	..	..	..	..	..	All	All	Only few
F_4	1156	1011² soft bl.....	..	..	..	..	..	..	All	All	Only few
F_5	1206	999² soft bl.....	..	..	..	..	All	All	..	..	Normal fertility
F_5	1318–19	1206² dp or not.....	..	..	..	..	All	All	..	..	Normal fertility
F_5	1250	1150².....	..	..	..	..	All	All	..	..	Stock

blist father in one of his second chromosomes not containing px. Thus both bran and soft blist without px were obtained and produced perfectly fertile stocks, as opposed to the same combinations with px. But the F_2 ratios again were strange. (The extracted bran and soft blist stocks behaved in accordance with expectation in outcrosses, though the ratios for the bran and soft blist classes were not always perfect.) No. 715 segregated as if the cross had been bran/+, poi/+ × bran/bran, +/. The expectation is: ♀ ½ bran ½ +; ♂ ¼ poi ¼ bran ¼ soft blist ¼ +. If we are willing to accept the numbers in general, the result is nearly obtained, but all males poi and not bran are missing, i.e., lethality in the presence of heterozygous bran px, and that only in the simultaneous presence of poi. Though one of the parents must have been bran, it was not recorded, though so unobtrusive a feature as the heterozygous plexation had been noted. It is therefore hard to believe that bran had been overlooked. F_2 717 must have had both parents bran, and finally, 716 segregated soft blist and also px and no bran. As it is inconceivable that bran was not seen in 716 but was seen in 715 and 717, checked within the same hour, we must assume that here as well as in a former similar case bran was somehow suppressed in the phenotype (or had arisen as a mutation in the germ line only?). No final explanation can be offered. The table shows in 716, 717 a few females soft blistered which are clearly not expected (all females heterozygous for poi). There is a strong suspicion that once more the bran locus had mutated.

One more pedigree may be added in which both soft blist and the same with px appeared in the same brood, the former being viable and selected for establishment of a stock which has bred normally for six years since, whereas the latter was almost sterile. From the same bottle from which the parents of the former crosses were obtained, a rather low px female was crossed to a soft blistered male. Table 142 contains the results.

F_1 578 shows that the px mother must have been heterozygous for bran (second chromosome) and poi (first chromosome) in order to produce ½ soft bl offspring, i.e., the cross was px bran/px, poi/+× bran/bran, poi. Four classes of offspring were expected: (1) px bran/bran, poi/poi (♂ poi); (2) px bran/bran, poi/+ (♂ +); (3) px/bran, poi/poi (♂ poi); (4) px/bran, poi/+ (♂ +). Of these, no. 1 (soft bl) and no. 4 (+) alone were present, i.e., the combination px bran/bran (= broad) was not viable without poi chromosomes, and the combination px/bran was not viable with poi chromosomes. F_2 from both parents no. 1 (soft bl) ought to be all soft bl with one-fourth px. Actually (712), in both classes, without and with px, about one-fourth (a little less) of the flies were neither soft bl nor broad, but + and px. This would require that another chromosome be heterozygous in the parents for something which suppresses the bran effect (and therewith soft bl). A similar feature has already been described in the former case. Unfortunately, no analysis of these extra classes was tried at the time, but if bran is a small deficiency produced by nonreciprocal translocation, the duplication would act as an inhibitor and would be expected to be present when bran is newly formed. Another F_2 (713) ought to have given the same results. Actually, there was a segregation of not px : px = 2 : 1, and the two unexpected classes + and px contained only a few individuals. The ratio of 112 : 7 = very near 15 : 1 may be significant, but it is possible also that the seven not soft bl flies were the product of an autosomal crossing over, involving the inhibitor, though this is difficult to imagine. The third F_2, no. 714, was stranger

still. There were almost no soft bl females, which looks as if all females but 4 out of 95 contained the inhibitor for bran. The males were all but one soft bl, but ¾ of the males were missing. This shows that the X chromosome was also involved. It is very difficult to give an interpretation of these data in concrete terms, as the unexpected classes were not analyzed at this stage. One thing is certain, namely, that a complicated relation between the second chromosome, involving px and bran, the first chromosome, involving poi, and some other locus and at least another autosome were involved in the happenings which produced low px and soft bl (= bran + poi) out of px bl. It is further remarkable that no broad angular = bran was segregated. In both former groups bran was obtained in F_2 or F_3 after crossing soft blistered to one of the other types from the same line. As the original mother here had been px, as was also the case in the first group, the px chromosome alone cannot be responsible. Soft blistered with px produced from these crosses was almost sterile (1009, 1011, 1154, 1156). But one soft blistered female (713) was crossed to a soft blistered male of unrelated origin (715, a cross which had produced bran; see table 141), and from this cross a fertile stock could be immediately established in the absence of px. Again, the px chromosome was involved in the sterility and unviability of soft bl containing this chromosome as well as the suppressor of broad, the latter obviously being involved both in the sterility and in the unexplainable ratios. Though we cannot propose any concrete interpretation, I can hardly see that one could be derived which would not be based upon the consequences of small translocations involving probably three chromosomes, translocations of the type actually found in the genetic analysis presented above.

When the pointed singed flies had appeared, as reported in the last section, after outcrossing, the combination bran px/bran px was segregated (see p. 494). This was almost sterile and a stock soon died out. As the X chromosome (derived from Oregon wild) did not contain poi, it follows that the sterility just discussed for the soft blist px combination is due only to the bran px combination, and we point again to the salivary analysis of these loci.

Only one more case of mutation within a stock involving the known loci may be described. In a true-breeding soft blistered stock (= bran/bran; poi), no. 5085, a single female was found with one wing normal, the other truncated, and, in addition, a dark trident on the thorax. This female was crossed to a pointed male and all offspring were pointed, but half of the sons were missing. In F_2 from this, not only poi and soft blistered segregated as expected, but also bran, which turned out to be a new bran allele which, with poi, produces long but soft and blistered wings. Bran could only segregate if some poi gametes had mutated back to normal. The dark trident also segregated and turned out to be an ebony allele. Thus a new bran allele had appeared in one female, together with ebony and, as it seems, a mutation from poi/poi to poi/+. The sons with the return mutation X (+) were lethal. But in the offspring of the daughter, heterozygous for the poi from the stock and a standard poi, a part of the poi X mutated back to normal, but apparently only in the gametes simultaneously containing bran (bran/bran, poi/+ flies and not bran/+ or +/+, + flies).

e. MUTATION IN THE LINES svr^{poi} AND px bl

We have reported above that in an inbred stock of svr^{poi} a bran or a soft blist (bran/bran, poi) individual is occasionally found. Once we succeeded by chance

in finding a svr^{poi} female which had become heterozygous for bran by mutation, with simultaneous mutation of svr^{poi} into svr$^{poi\ s}$. Many crosses of svr$^{poi} \times$ bw sp ba had been made with normal results. But in one such cross half of the sons had soft and partly singed wings. We already know (see table 74 of phenotypes) that the allele svr$^{poi\ s}$ in the presence of heterozygous bran produces such a wing in some individuals, the homozygous combination being soft blistered. Actually, F_2 segregated, according to expectation, bran and soft blistered and soft singed like F_1. (It is remarkable that the segregants combining bw sp ba with poi s were extremely blistered, blisters never being found in this bw sp ba stock). Thus, the poi mother had been heterozygous for the mutants bran and poi s, both of which had not been found among the other poi flies.

We have mentioned above that the mutant svr$^{poi\ s}$ has occasionally cropped up in the px bl stock and spread through it. One should expect the same for bran. But whereas bran homozygous together with px is poorly viable, it might not survive at all in a stock bottle. Special tests made for the presence of bran in px bl were

TABLE 143

	Cy Sb	Cy	Sb px bl (few not bl)	px bl (few not bl)	Sb	Cy px
♀.....	25	10	12	8	1	..
♂.....	24	24	16	8	3	1
Exp.....	4	2	2	1	C.o.	C.o.

always negative. Only once, namely, at the time when poi s had spread in the stock, as described above, was bran discovered by chance. A considerable number of crosses px bl $\times$ Cy/Pm, Sb/H were made in both directions and with blistered as well as not blistered flies. From these, many different F_2 were derived. In one of them, F_1 569 Cy, Sb $\times$ F_1 562 Cy, Sb, both from highly blistered parents (mother in 569, father in 567), most of the segregating offspring with the original second chromosome containing px were again plexus and blistered, which we know is not the case in other F_2 involving px bl. The actual segregation is given in table 143. The considerable amount of crossing over between Cy and px is unusual. The plexation was extreme, since Sb usually acts as an enhancer. The wings were long, not short as in soft blistered. In the next generation from px blist flies (with and without Sb) only plexus blistered flies were obtained, but now they had low plexation with or without Stubble. These bred true for soft blistered plexus, which was more or less sterile and a stock died out. This shows that both original parents had not only contained poi but were also heterozygous for bran, which explains their stronger blistering. By chance, one of the F_2 bred from both F_1 was made from F_1 parents Cy/bran px, as the further offspring revealed. We have found by tests that the enhancing action of the Sb chromosome upon px expression is due to a simultaneously present inversion. Obviously, this enhancing action also prevented the shortening of the px bran poi wings. It cannot be explained why the enhancing action was lost in F_3 and F_4 and the soft blist px type became visible. There is a possibility that another poi or bran allele was involved. We remember that bran px + poi is phenotypically soft blistered plexus, and bran px + poi s is soft blistered spread plexus. The some-

TABLE 144

CROSSES WITH yellow INVERSION AT THE TIME OF RETURN MUTATION OF px bs

Gen.	No.	Cross	♀	♂	New mutants
F_1	3696–98	poi × y-Inv.	As expected.	As expected.	
	3710–11	poi h × y-Inv.	As expected.	As expected.	
	3746–47	px[a] × y-Inv.	29 px (15 bl), 46 +.	33 px, 22 +.	
F_2	3812	3696[2].	78 as expected, 1 poi:dp.	87 as expected.	bran[dp]
RF_2	3940	3746 + × px[a].	½ px, ½ +[b].	½ px, ½ +[b].	
RF_2	3941	px[a] × 3746 +.	45 extr. px bl, 64 "low px".	49 extr. px, spread, part blist., 28 poi bl, 23 +.	poi bl, bran
RF_2	3942	3747 px bl × px[a].	103 extr px (½ blist).	50 extr. px, 18 ditto y, 16 y low px.	
RF_2	3943	px[a] × 3747 px bl.	47 ♀ px (part bl), 2 ♀ low px.	55 px.	2 ♀ mut. px/px→ px/+
RF_3	4528–29	y × 3941 px spr bl.	Short bristles.	19 spr bl, 21 + blist, 6 +.	blist
RF_3	4530–31	y × 3941 +.	Normal.	Normal.	
RF_4	4693	4529[2] ♂ spr bl.	Normal.	½ + , ½ blist.	
RF_4	4695	4530[2] ♂ +.	.	+, 1 px.	px return
RF_4	4696	4530[2] ♂ +.	.	47 +, 4 px.	px return
			SELECTION IN I(1) $y^{px\ bl}$		
F_1	3949	y + from bottle.	67 +, 1 px bl, 3 low px, 3 dwarf, 1 dwarf low px.	60 +, 5 low px, 5 dwarf, 1 dwarf low px.	dwarf and px segr.
F_2	4532	3949[2] low px.	61 + and short bristles.	77 + and bristles short.	
			6 px and px bl, norm. br.	18 px bristles norm.	
F_2	4533	3949[2] dwarf px.	62 high px (13 blist), 49 +.	48 high px; 30 +.	
F_2	4534	+.	+.	+.	
F_2	4535	+ very large.	+.	+.	
F_3	4707 etc.	4532[2] +.	Not px : px 3 : 1.	Like ♀.	
F_3	4728 etc.	4532[2] px.	All px and blist.	Like ♀.	

[a] y stock px extreme from poi × poi h
[b] px/+ like low px.

what different phenotype here may therefore have been based upon other alleles which could not be tested on account of the sterility of the combination. The pointed allele appeared more like soft in such combinations (without bran, px, Cy) as could show it.

We have reported above the origin of the Inv(1)$y^{px\ bl}$ as a single male in the px bl stock, and we stated that in the homozygous stock of this inversion individuals appeared heterozygous for px and bs (by return mutation) from which an Inv(1)$y^{px\ bl}$ stock without px and bs was isolated. When this happened a not px pair but Inv(1)$y^{px\ bl}$ from the bottle in which the return mutation had occurred was bred. The offspring consisted of 127 +, 9 low px, 8 dwarf, 2 dwarf low px (both sexes alike). The parents were obviously heterozygous for px, but the segregation for px was about 12 : 1 instead of 3 : 1, and, in addition, dwarfs appeared. This shows that the return mutation was hardly the simple event implied by the name. A pair of the low flies (all y-Inv) produced 61♀ 77♂ normal, but with bristles varying from shortened to very short; further, 6 ♀ px (3 blist) and normal bristles, 18 ♂ px, also normal bristles. What had looked like homozygous px was again heterozygous, and 1/11 ♀ and about 1/5 ♂ px segregated, the not px flies having abnormal bristles—again, not a clear or normal behavior. The px dwarfs also produced a segregating offspring, all large, not giant, all with normal bristles, namely, 62 ♀ px (12 blist) 48 ♂ px, 42 ♀ 29 ♂ +. Crosses of + with dwarf were normal. In the following generations px segregated, where heterozygous, quite normally, and + bred true or was px/+. Extracted px had the same phenotype as was originally found in the stock.

Simultaneously, a y-Inv male was crossed to an extreme px from the stock which had been derived by mutation from poi × poi h (see p. 480) and which did not contain any more poi, but bs^{pp}. F_1 segregated into px with and without blisters and normal or hetero-px flies, one-half of the males of the latter class missing. The father thus had been px/+. There were no poi ♂ or ♀. Normal females were backcrossed in both directions to the px parental line. The offspring segregated into strong px and heterozygous px of a much higher grade than normal, a result of the simultaneous presence of the bs^{pp} derived from the mother. Moreover, about one-fourth of the males were typical pointed blistered not px flies, which requires the presence of bran and poi bl, neither of which had been present in either parent. One-half of the males were strong px and spread, some blistered. (In a reciprocal cross, also, two females among 49 showed a return mutation to px/+.) A test of these males with y females produced spread or not spread and blistered males, whereas all females had short bristles. The X chromosome thus did not contain poi, but another sex-linked mutant causing the spread blistered wings. This type was inherited as a simple sex-linked character, but was later lost. The normal brothers of the spread blistered males from the first y × spread blistered cross gave only normal sons with y mothers. But twice a few px males segregated, once 4 among 51 (2 of them combined with the marker ey) and once 1 among the same number; thus px had again returned. Finally, a cross of poi × the same y Inv, which had become heterozygous for px, threw in F_2 1 poi : dp ♀ among 79, meaning a mutation to $bran^{dp}$. Further tests of all these features did not furnish any more information. Table 144 presents the foregoing data.

These detailed descriptions may suffice. Corresponding cases contained only in the tables followed the same pattern.

TABLE 145

ORIGIN OF rudimentary

Gen.	No.	Parents	+		poi		rud		low px		px bl		
			♀	♂	♀	♂	♀	♂	♀	♂	♀	♂	
P	4203 B	px bl	..	..	..	..	..	..	..	..	All	All	
F_1	4474 B	px bl × px bl	136	70	..	..	..	1	18	19	..	..	
F_2	4610 B	+ × +	185	80	..	..	..	37	..	..	..	..	
F_2	4612 B	+ × +	151	..	..	65	..	55	..	..	..	..	poi partly + ?
F_2	4613 B	+ × +	8	3	..	..	..	1	..	..	..	..	1 ♂ dwarf
F_3	4764 B	4612² ♀ + × ♂ r	77	..	..	43	29	34	25	15	..	..	
F_3	4765 B	4612² + × +	199	67	..	?	..	49	2	..	..	..	+ and poi not classifiable
F_4	4988 B	4764² px × px	..	..	..	..	..	24	77	42	..	..	9 ♀ 7 ♂ px poi, 1 ♀ 3 ♂ px spr bl
F_4	4977 B	4764² + × poi	73	35	45	19	..	41	43	29	..	..	
F_4	4978 B	4765² + × r	28	53	44	13	..	71	70	..	..	..	
F_5	5178 B	4988² px poi × px spr bl	..	..	..	..	..	10	37	12	..	..	57 ♀ 27 ♂ px spr bl, 5 ♀ broad round
F_5	5173 B	4977² px Mass	..	..	..	..	..	14	132	33	..	..	4 ♀ 3 ♂ poi px, 9 ♀ px spr bl
F_6	5348 B	5178² px × px	..	..	..	..	..	16	110	125	..	..	85 ♀ 69 ♂ px high, 40 ♀ 15 ♂ px spr bl
F_6	5352 B	5178² px spr bl × r	..	..	..	..	13	14	10	6	..	..	34 ♀ 44 ♂ px spr bl

f. THE MUTANT rudimentary

A short discussion of the origin of rudimentary will show features comparable to those discussed thus far. The first appearance of rudimentary as a single male out of 90 simultaneously with the complete change of the px bl type has been recorded on p. 294, and also in table 1. Table 145 contains the data for the first generations, the first rudimentary male not having produced any offspring. (Most of the data have already been given in other tables.) A new appearance of rudimentary males in the offspring of the same line occurred twice later. From no. 4610 B a true-breeding normal (+) line was isolated. Four generations later, two females from this inbred line, which had not thrown any rudimentary males, were crossed to a second-chromosome marker stock (quintuple) and also to a third-chromosome one (rucuca). No rudimentary flies appeared in F_1. But two of the backcrosses of F_1 females with the marker-stock males produced among a large number of males a few rudimentary, namely, in the second-chromosome cross 1 ♂ rudimentary and speck, in the third-chromosome cross 4 rudimentary males in the classes triple, ru h, and ru c. The crossover classes might be chance, but it is remarkable that both sp and the ru h region are also involved in the twin mutant pointed (see above). A few more instances of the reappearance of a few rudimentary males in the descendants of the px bl stock have been found. As an example I mention a cross $\underline{y} \times$ px bl. In F_2 (no. 300) one rudimentary male among numerous normal ones was found. In other such cases the rudimentary male did not breed and therefore could not be counted with certainty as a mutant. But it is remarkable that, unlike bran and poi, rudimentary has not reappeared frequently, though it is regarded generally as a rather unstable locus.

As table 145 shows, the first rud males appeared after the manner of a mutant simultaneously with the disappearance of px bl from a whole brood. But as three out of four broods from normal parents of this F_1 produced rudimentary sons, many of the females in F_1 must have been heterozygous for rud, which, then, was in some way produced in many gametes of the father of F_1 but only in one egg of the mother, though it is also possible that only the mother was involved and only one rud son survived because of some lethal condition. Actually, one-half of the + males are missing in F_1, which may have been the rud males, lethal because of something else in the X chromosome, which was removed in one male by crossing over. It is remarkable that in one of the F_2 the rudimentary males are only ½ of the normal brothers, again indicating a lethal class. In F_3 from the wild type in F_2, half of the males are missing in the rud class as well as in the plus class. In F_3 from $+ \times$ rud, the plus female turned out to be heterozygous for rud, and correspondingly rud females and males are produced, but not in one-half of the offspring; actually more than one-half of the expected rudimentary individuals are missing. This might seem to be a question of viability, but we shall see later that this is not the case. Some of the data of table 145, such as F_4 4978, show the expected one-half rudimentary males, so that some combination with something lethal is involved, presumably a combination with another chromosome. F_6 5348 is another instance. Here the rudimentary males are only about ¼ of the males; and in F_4 4977, again the rud males count exactly one-half of the expected number. It is hardly possible to reconstruct from these facts the first appearance of rudimentary. If we call it a

mutation in one of the X chromosomes of the mother of the line, we are confronted with the fact that other things happened simultaneously which made the same X chromosome unviable in certain combinations with one or more autosomes. One more fact ought to be mentioned. When rudimentary males were first produced in numbers (4610, 4612), each of the two broods contained one rudimentary male with some extra features never since observed, namely, a pathological combination of wing, leg, and antenna-like structures on one side of the body. (Both males were sterile.) This might have been a chance occurrence, but it might also have been a rarely surviving deficient or duplicated condition found in connection with the whole process of "mutation."

When it first appeared, rudimentary still contained the plexus blistered constitution which otherwise had disappeared. The rud individuals in table 145 ought, therefore, to be classed also under px bl. When bred with attached X yellow (y), px and px bl segregated among the y flies. A first test with standard rudimentary (r) showed the new rud to be an allele of r, which ought to be called $r^{px\ bl}$.

The other important fact regarding the origin of rudimentary is its production simultaneously with pointed during the same set of changes. Two of the three F_1 + which threw rudimentary sons simultaneously produced one-half pointed sons. These plus females, liberated from the px bl phenotype by some change, then had one X chromosome with pointed, one with rudimentary. But we shall see that the rud chromosome also contained pointed. A poi type in the mother was possibly overlooked since the mutant had not yet been discovered. But it is also possible that both poi and rud had originated simultaneously in one chromosome for which the mother was heterozygous and therefore normal, and that both loci, distant 57 units, showed almost complete crossing over with only a few noncrossover normal flies. It is further possible that the mother of both poi and rud had been a crossover fly from a crossover in a former generation in which heterozygous poi and rud had arisen in the same chromosome. (It must be said now that a ♀ poi/poi r looks like poi, but females and males poi and rud both homozygous or hemizygous are phenotypically rud).

The mutant has since been bred over y for many years. For a long time the type was constant; later it varied considerably. At present only one stock remains as it was, with short blistered wings, still containing pointed. Other stocks show perfectly normal wings, but outcrossed to heterozygous r/+ females they produce rudimentary daughters. Obviously another allele of r has arisen with long wings and better viability. Modifiers are not responsible for this type. (Rudimentary alleles with normal wings have been described before.) In other bottles other types appeared, such as long dumpy-like wings, wings half-long and lancet-like with isolated tufts of marginal hair, and others. We shall return to these types below. Only plexus and blistered could be removed from the rudimentary wings, but blistering remained in the short-winged type owing to the presence of pointed. The phenotypes of combinations of rudimentary with pointed and bran are:

bran/bran, poi $r^{px\ bl}$/poi $r^{px\ bl}$ = short rudimentary blistered
bran/bran, poi/poi $r^{px\ bl}$ = soft blistered
poi $r^{px\ bl}$/poi $r^{px\ bl}$ = rudimentary short and blistered; but some flies with an epistasis modifier vary from pointed via pointed with a few marginal hair at tip missing, via pointed with a slightly sinuated tip, and via all transitional stages of truncation to truncated or dumpylike
$r^{px\ bl}/r^{px\ bl}$ = dumpy or even normal
poi/poi $r^{px\ bl}$ = pointed and part blistered

Rudimentary together with pointed gives the short blistered rudimentary wing. It thus shows an epistasis over pointed, as is found also with other loci with a truncating effect, such as bran[2], and it also produces the characteristic blistering effect. The latter is even visible with low penetrance in the heterozygote poi/poi r. A semi-dominant modifier was found which shifts the epistasis toward pointed with all transitions which resemble (though they are not completely identical) the ll-bran combinations described above. Rudimentary has many other remarkable features, but as they are also found in other rudimentary stocks their discussion does not belong to the present subject and will be presented independently.

4. Mutation after Outcrossing px bl and Its Derivatives

Though the stocks of px bl and its derivatives were carefully watched, mutation in the stock bottles was rarely found, if we consider now other mutants than those at the svr, arc, px, and bs loci. This does not mean much, since recessive and poorly viable mutants are swamped in stock bottles. Dominant and rather viable mutants were also absent. There were also many long series of inbred pair matings made with different stocks, and again no mutants were found, which shows that the general mutation rate apart from the phenomena already described is the usual low one. But when px bl and its derivatives were outcrossed or crossed among themselves, dominant and recessive mutants appeared in significantly high numbers and in many cases in a way which excluded their presence in heterozygous condition in the stock. A quantitative evaluation is, however, extremely difficult, except for dominants, because many of the recessive mutants have incomplete penetrance and therefore may have been present before they were found. Moreover, the possibility of long-continued breeding of heterozygotes with normals is not excluded in an experiment of normal size not planned with special detecting methods.

To describe one case in detail: The only mutant not affecting the loci studied thus far which was isolated from px bl stock in many years of breeding is a small inversion with one break in the yellow region (see salivaries, text fig. 4), $T(1)y^{px\,bl}$, with the appearance and behavior of a yellow allele (see p. 398). It was found as a single male in px bl stock. We have already described how it reverted later from px to normal without a change in the X chromosome, and a stock was kept as y-Inv without px. In the hope of reproducing this event we bred for six generations 30 pairs in brother-sister matings, altogether about 45,000 flies, without a single mutant appearing. Nine months later a series was started by crossing 10 pairs of Bld-T with this y-Inv and backcrossing in each generation heterozygous females recognized by Blond, with y-Inv males. In ten generations totaling 3,263 ♀ 3,774 ♂, a mutant "spiny legs" (sple) was segregated four times, in irregular numbers. In RF_4, 4 ♀ 6 ♂ among 59 ♀ 58 ♂ appeared. In another F_7 they appeared in Mendelian numbers. This F_7 was derived from the same RF_2 and a divergent line thence; a third time, in RF_9, 7 ♀ 5 ♂ appeared among 33 ♀ 34 ♂; this, again, was derived from F_4, which had given the second case in F_7 in another line of origin. Finally, a fourth appearance was only 2 ♀ among 70 in RF_9, which in RF_4 had been branched off the line of the last case. Now, in the first case and the stock established from it the character had very little penetrance; in the second case it was expressed very strongly; the same was true in the third case; and in the last case it was extremely strong, with additional features (see description below). It turned out that three different

alleles were involved, a very low, a medium, and a high one. Now, the common ancestor of all four was one RF_2 which gave rise to three out of ten lines; but by the chances of breeding in following generations this line was selected for propagation. Now, had the original pair been heterozygous? Was the mutant carried along and only rarely given a chance for segregation? This is hardly probable. In ten generations, which in time became more closely related by selection of one of the original lines, only 4 among 83 broods (with an overall expectation of 21 in case of former presence of the mutants) segregated the type. Furthermore, the expression of the type was very strong on two occasions and could not have been overlooked otherwise, and in one of these cases, the extremest type, only 2 among

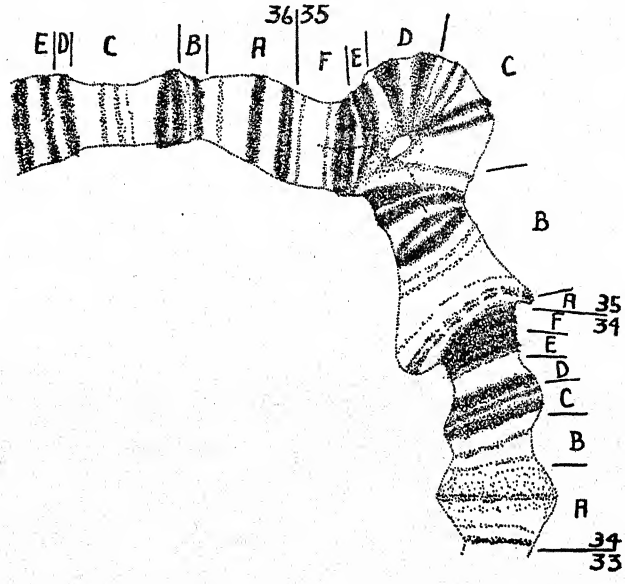


Fig. 4. Black deficiency (dominant black). M. Kodani del.

70 ♀ appeared. Thus the case is rather good for two or three independent mutations after crossing.

There are a few more remarkable features of this case. We add at this point that the localization of the mutant called sple gave it a location of 5.5 units to the right of black in the second chromosome, i.e., at 54. In *DIS* 16, P. T. Ives described a mutant tarsae (*sic*!) irregular-ti at 2–55.9 found in wild type. It is possible that our sple is allelic with this. A crossover experiment with c (75.5) gave 16.2 per cent, i.e., location at 59.3. (The latter test was made with 1,189 flies.) The lower alleles were not checked immediately for the salivaries. Meanwhile, the stocks of the lower alleles had become phenotypically identical with the highest allele (disheveled hair, etc.). A selection of modifiers is improbable since the original tests had agreed with multiple allelism. Thus we must assume that the high allele had originated as a mutant in the low stock and spread here. Actually, this allele shows simple segregation without much variability, thus demonstrating its nature of a multiple allele. The salivaries of this allele were, so far as could be ascertained, normal both to the left and the right of the spindle fiber (s.f. at 55).

In the same line another mutant appeared which could be proved to appear repeatedly, namely, a dominant. The phenotype was similar to dachs but differed in the extreme hairiness of the dachs legs (possibly a combination with spiny legs) and broad, blunt, arched, and spread wings. The mutant was so weak that it always died in the mating vials without offspring. It appeared in the tenth generation of the series as 18 ♀ 19 ♂ among 60 ♀ 70 ♂, both Bld or y-Inv otherwise. This looks more like a recessive. But when, soon afterward, a mass backcross was made of standard yellow with our y-Inv backcrossed to yellow, 13 among 603 flies were of exactly the same dachs type, thus revealing its dominance (all chromosomes were heterozygous with those from standard yellow). Some time later, 1 ♀ 3 ♂ were found in the y-Inv stock. This, then, is certainly a recurrent dominant mutant. All the facts in this case point to a rarely realized or surviving deficiency duplication from translocation. No test was possible, as the type never occurred in crosses with recessive markers.

Furthermore, in the line of crosses under discussion, nicked wings were found which were inherited in an irregular way with low penetrance, and which could not be isolated. These are, then, five mutants produced in numbers which cannot be determined reliably in about 7,000 crossbred individuals, as opposed to none among 40,000 in the controls.

We had found a number of comparable cases, actually almost in each case in which px bl or one of its derivatives was crossed, and many generations of the offspring were bred (for other purposes than producing mutations). The following example will be given in detail because dominant mutants make it favorable for study (see table 146). This line begins with two reciprocal crosses of pointed blistered stock, long inbred, to Blond translocation (nos. 3920–23). Poi blist, we remember, is the combination of bran in the second chromosome with $svr^{poi\ bl}$ in the first chromosome.

In F_3 two certain and one probable mutant appeared, namely, dachs (d) and the dominant Bran, which has already been analyzed (see p. 356). There was, further, sooty, which, however, was lost and therefore is dubious. In one of the five identical F_1 the dominant Bran appeared in a strange way, discussed above (p. 360). F_2 from this (see pedigree, table 146) had in one brood 2 dachs ♀ among 72, also one ♂ with abnormal abdomen which was irregularly inherited and could not be extracted, and 1 gynandromorph. The last-named must have had a genetical basis, since one sister brood also contained a gynander and a third one appeared in a later generation—altogether too many for a chance result. In addition, one sister brood had 9 sooty ♀ among 34 which turned out to be e^s. In one F_3 with a rather unusual sex ratio, bred from one of the gynanders, dwarfs (2 ♂ among 76) appeared which inherited the character irregularly. In F_3 of the parallel cross, dachs also segregated in two broods unrelated to the former. Further, 3 ♂ among 24 were bran blistered, which contains both another bran allele ($bran^2$) and a poi allele poi sq (isolated from this cross).

In F_4 of the first line in an outcross designed to test the Bran-poi bl combination (phenotype dumpy blist) among the segregants of this type (4966, 13 ♀ 10 ♂) there were 4 ♀ with rough eyes and bristles somewhat resembling forked. They were mated to soft blist brothers and produced Bld and soft blist offspring; the next generation contained 9 such ♀ (no ♂) among 75 Bld or soft blist. (Another F_6 from 4966 contained a single such ♀ among many ♀.) They were mated for analysis, but did not

TABLE 146

PEDIGREES

F_1	3922 poi blist × Bld All daughters Bran/Bld (*dom. Bran*)	3736 poi bl × Bld
F_2	4512 Bran/Bld × poi 2 ♀ *dachs* among 72; 1 ♂ *abn. abd.*; 1 *gynander;* 1 ♂ abn. wings 4539 Same cross, 9 ♀ *sooty* among 34 4511 Same cross, 3 more F_2 4511 Same cross, 1 *Gynander*	3736[2] ♀♂ Bld. ♂ poi and (2) Df
F_3	13 F_3 and test crosses 4698 = 4512[c] Gyn × Bran 2 ♂ *dwarf* 1 poi abn abd.; 20 ♀ : 76 ♂	3966 Bld × Bld 3 ♂ among 24 *bran*[2]/*bran*[2], *poi*[sq] 3973 Same cross } 21 ♀ 17 ♂ *dachs* with Bld or 3976 Bld × poi } poi among 75 ♀ 96 ♂ 3 more F_3
F_4	4966 Bld × soft bl 4 ♀ among 81 *rough etc* (*M*) 4 more F_4	7 F_4 and test crosses
F_5	5101 (soft bl × r)[2] 8 ♀ *poi:dp* among 74 = *bran*[dp] 5103 Same cross, 1 ♀ *poi:dp* among 88 5 F_5 and tests	4814 = (♀ × soft bl)[2] 1 ♀ *snipped* (?) 3 more F_5 *Many dwarfs*
F_6	5180 (♀ × 5102)[2] 5162 Same cross, *triplo-X* 3 more F_6 and tests	9 F_6 and test crosses 5031 = 4813[2] dwarf dachs × dachs 1 ♀ 8 ♂ *slender* = bran[1]/bran[1], poi[s] among 14 ♀ 18 ♂
F_7	3 F_7	16 F_7 and tests
F_8	5294 = 5208[2] poi:dp 1 *Gynander*	5189 = 4813[4] 1 ♂ *Bidexoid* and dachs among 62 7 more F_8 and tests
F_9	5329 = 5294[2] poi × poi 2 ♀ N among 78 (*Notch Df*) 1 more F_9 (sister)	14 F_9 and tests
F_{10}	1 F_{10}	4 F_{10} and tests
F_{11}	5378 out of poi:dp 23 ♀ 5 ♂ with *bran*[r] 5 more F_{11} and tests	7 F_{11} and tests

reproduce their kind any more. They were, obviously, hardly viable Minutes. In F_5 of the parallel cross (4819) 1 ♀ with extremely scalloped wings—resembling Df(2)vg—and rough eyes was found among many. She was sterile.

In F_4, dachs had been crossed again with the stock Cy/d. In the offspring dwarfs appeared which were inherited rather irregularly. A stock could be established. In

F_8 when dachs segregated again, 1 ♂ dachs among 68 ♀ 62 ♂ had scalloped wings. From it a stock of a new dominant sex-linked mutant, Beadexoid, was derived. Another F_4 ♀ of the first line was tested by breeding to a rudimentary ♂ also containing svr^{poi} (from stock $r^{px\,bl}$). In one F_5, 8 among 74 ♀ were poi : dp, which we already found to be a specific combination of $bran^{dp}$ with svr^{poi}, i.e., bran had mutated to $bran^{dp}$. In another F_6, 1 ♀ among 87 showed the same type. In the sixth generation an unusual result was found. Soft blistered males of the extreme rudimentary-like type were crossed to an attached-X female, with the usual result (♀ y ♂ poi). Twice an F_2 of such a cross contained triplo-X females (not yellow, but also not normal in color, scalloped, rough-eyed, sterile). Once only, 3 among many females (but, once, half of a huge number of females) survived. The soft blist ♂ must have contained something which made triplo-X females viable (the chromosomes were checked in the ovary and found to be triplo-X). As this was not the case in numerous similar crosses, some mutant must have been present. Actually, in one case a y sister of the triplo-X females produced in the next generation again triplo-X daughters, and so did further generations as well as repetitions of the crosses. Once more the same thing happened when a soft blist and dwarf ♂ of the same origin as the former cases was crossed to y. Already in F_1, 1 triplo-X ♀ was obtained, and in F_2, 6 among 41! We did not succeed in isolating the condition responsible for survival of triplo-X, which must have been autosomal. Again, in F_9 bred from pointed flies, 2 notched females among 78 appeared and turned out to be an N deficiency. From the lines containing both N deficiency and poi : dp the new allele $bran^r$ was obtained and isolated out of poi : dp parents. In the other line in F_6 a brood from dachs and dwarf parents produced, in addition to the expected types, 1 ♀ 8 ♂ slender, which means mutation of bran to bran′ (or of + to bran′, bran not always being distinguishable with dachs), and from + to poi^s.

Thus, in this line of eleven generations, after crossing poi blist and Blond and selecting out Bld after four generations, the tested mutants Bran, bran′, $bran^2$, $bran^{dp}$, $bran^r$, poi^{sq}, poi^s, dachs, dwarf, Beadexoid, N-Df, and sooty were isolated; and the probable but not isolated mutants abnorm 4966 (M), "snipped," triplo-X enhancer, gynander-enhancer, abnormal abdomen were encountered, i.e., probably 17 (certainly 11) mutants among about 15,000 individuals. (An exact number cannot be given, because a great number of broods were test crosses for segregating or new types in which normal or expected results were simply marked without counts.) The pedigree (table 146) shows the two parallel lines with indication of only the first appearance of the mutants. As these appeared in direct lineage of the original cross as well as in offspring of outcrosses made to test segregating types (the series was made for the analysis of poi blist), the broods of each generation are not itemized except in the case of mutation.

One of the most frequent mutants derived from the different poi alleles in inbreeding as well as in outcrosses is contained in the phenotype one wing pointed, one wing dumpy (see p. 373), this poi : dp being a combination of svr^{poi} with $bran^{dp}$. The latter, then, is the frequent mutant, recognizable only in this combination. One of the stocks was isolated from flies reported in the foregoing pedigree. (For data on this see pp. 373 ff.) Among thousands of flies in this stock, occasionally one or a few soft blistered flies appear (never obtained thus far in pair breeding). During the analysis of this situation (see p. 379), which we may consider as a continuation

of the former pedigree, more facts belonging to the present section were found. Soft blistered in this case is produced by a mutation of bran^{dp} into bran or bran^{r}. The pedigree, then, started with bran^{dp}/bran^{r}, poi flies. In F_3 from poi : dp × poi, 10 out of 27 ♀ were N-deficiency, which was combined with poi and bran^{dp}. There were only 10 males, i.e., about ¾ of the males missing. The conspicuous deficiency, which could not have been overlooked in former generations, thus must have arisen in half (or more) of the eggs of the mother, which was bran^{dp}/bran^{dp}, poi/poi. In each generation the main types were tested with the markers bw e ey, without special results. One F_2 was obtained by backcrossing a special type which had segregated (with arched opaque wings) to a male of poi : dp stock. One female and male each of the poi : dp type were tested against the marker stock. In both cases all daughters were sooty, rather dark; e^{s}/+ had changed its dominance, very pronouncedly in the females, less so in the males. This dominance-enhancer was inherited to the next generation and could be recombined as an autosomal dominant with homozygous e. Such flies were extremely black, showing that the action of the enhancer was more that of an intensifier for ebony. In the same generation one brood was extracted from F_2 parents bran^{r}/bran^{r}, poi/poi × bran^{r}/bran^{dp}, poi (phenotype: rudimentary blistered varying to soft blistered). It bred true, in accordance with expectation, but one male poi : dp appeared, i.e., a return mutation from bran^{r} to bran^{dp}. Again, in the next generation F_4 from (poi : dp × bw e ey)^{2}, one of those containing the new ebony enhancer, 2 among 87 ♂ were bran, which means that bran^{dp} had mutated into a higher bran allele. One more doubtful mutant, arched opaque wings, segregated in a few individuals from different generations and was linked with the second-chromosome marker. After breeding true it completely disappeared from an extracted stock and might have been a chance modification, not a mutation. Finally, in a further outcross involving this arc opaque type 1 ♀ giant among 28 appeared (heritable).

One more characteristic case may be mentioned. A pointed blistered female (= bran/bran; svr$^{poi\ bl}$) was mated to lanceolate speck (ll sp), and F_1 males backcrossed to pointed blistered. It turned out that the ll sp father had been heterozygous for a second-chromosome dominant, lethal when homozygous, which produces shortened bristles of a bobbed or achete phenotype and very variable expression. Hence in the backcross the pointed flies showed this bristle character and the poi blist (= bran/bran) flies did not. Three out of 100 males, all with the intact pointed chromosome, were forked, which bred true as a forked allele with reduced fertility and an irregular heterozygous effect which had an interaction with the second chromosome bristle character in so far as females heterozygous in both had short, stiff, stubble-like bristles. Later the second-chromosome character was transferred by crossing over into the bran chromosome, as shown by poi blist and short-bristled flies, and segregation of ll sp, which could not segregate before because of the lethal dominant. It is quite possible that the forked mutant had nothing to do with the presence of the dominant, though the coincidence is remarkable. Two generations later, svr$^{poi\ bl}$ mutated back to normal in a chromosome containing the new forked. The mother had been svr$^{poi\ bl}$ f/svr$^{poi\ bl}$, the father svr$^{poi\ bl}$ f. The offspring segregated into 31 ♀ 32 ♂ pointed f and 28 ♀ 38 ♂ forked, but 7 ♀, i.e., ⅛ of all ♀, were not poi, likewise 21 ♂, i.e., ¼ of all males. One of these males was a dwarf. All the f flies tested were sterile, so that a further analysis was excluded. Again, a few gen-

erations later, in a large brood all poi blist and half of the males forked, bred from poi blist flies with heterozygous f, there appeared 5 yellow males, 1 without, 3 with forked, and 1 with abnormal abdomen. Pointed is not visible with yellow, but since the poi blist character was present it had not changed; the combination, with and without forked, must have been due to crossing over poi–f, which shows that the mutation had occurred in an early ovogonium. All yellow flies were sterile; hence we do not know what happened at this locus. Again we find interrelations which are not clear but are hardly based on pure chance. Nothing could be found in the forked region of the salivaries.

These examples of the type of happenings may suffice. These and some other such series are summarized in table 147, which shows that in these cases about one mutant in 1,000 flies was found, ¼ of them at the bran and poi loci and about ⅙ dominants. This of course is not a quantitative result, since the experiments were not planned for this purpose, and the pedigrees used for table 147 were selected because they showed the high rate of mutation. It should be noted, however, that although they are not fit for a measurement of mutation rate, they are certainly highly significant in themselves.

The same argumentation applies to the following data. A great many individual mutational steps were found in F_1 or F_2 of crosses with px bl and derivatives, but there were many more such crosses which did not yield mutants. Again, the positive results are significant for our problem without being quantitative.[14] Table 148 contains the data. Among the mutants contained in this and the other tables only one suggests that it had been present in the tester stock in heterozygous condition, namely, dachs. This segregated three times after crossing with Blond translocation in F_2 or F_3, once in two individual F_2. If d is present in the translocated chromosome it remains balanced in the stock, but may come out after crossing via crossover (d is far away from Bld in the second chromosome). In this case it might also segregate the same way in surviving Bld(1)Df females which have the two not Bld chromosomes. It is remarkable that occasional individuals appear with slightly bowed legs, like beginning dachs, though I never found dachs. This low type, which I recorded as half dachs, segregated also in these Bld crosses, either alone or together with real dachs; in the first case the real dachs appeared after a few generations. The low dachs neither bred true nor produced dachs in a compound with standard dachs. It looks like a low allele with extremely low expressibility. The real dachs, however, was never obtained in other numerous outcrosses of Bld, including a large control series, backcrossing ten pairs over and over to Canton wild. Thus it looks as if the real dachs from Bld were another allele produced in the crosses with poi and bran from the low allele sometimes present in Bld. (The real dachs bred true, though it is highly infertile, and gave a dachs compound with standard dachs.) It may be significant that dachs was obtained twice in other crosses than with Bld.

In many cases the chromosome which had mutated after crossing could not be assigned to those of the original parents, for lack of markers. But sometimes it was possible. Thus the N-Df in 2 ♀ among 74 in table 148, no. 13, occurred in the ec br chromosome after crossing to a male containing poi in the X and ro op (another mutant) in the second chromosome. Such facts seem rather significant.

[14] Quantitative experiments were started as soon as the progress of this work permitted. Sickness twice caused their abandonment. They have been started again.

TABLE 147

MUTATION AFTER CROSSING

No.	Cross	Gen.	No. broods	Number		Mutants			
				Flies	Mut.	Certain		Probable	poi, bran, px, bs⇄
						Not isolated	Isolated		
1	poi^{s} × bran blist	3	30	3,251	2	1 poi suppr.		1 M.	1 bran→poi
2	slender × bran blist	4	12	± 800	2	1 modif. for soft bl		1 y curled	
3	poi blist × ll sp	10	29	± 3,000	3	1 y	1 f		1 poi bl→plus
4	slender × poi	6	9	± 700	2	1 shaven depillate	1 giant		
5	slender × a px sp	3	5	± 500	2			1 M; 1 dwarf	
6	y-Inv × Bld	10	83	7,037	5	D	sple, 3 alleles 4 times		
7	poi bl × Bld a	11	140	±15,000	10	M_1	N, d	Gyn.; abn. abd; dwarf; triplo-X-mod	Bran, bran^{dp}, bran^{r}
8	poi bl × Bld b	11	..	.....	7	.....	d, dwarf, Bidexoid	snipped	poi^{sq}, poi^{s}, bran^{2}, bran^{1}
9	poi:dp from 8 (soft bl)	8	74	± 4,500	6	e-enhancer, giant.	N	ap. arch?	bran^{dp} return, bran^{r}

TABLE 148

MUTATION AFTER OUTCROSSING OF px bl AND DERIVATIVES

No.	Mutant	Cross	Numbers	Remarks
1	dachs (d) two alleles	(bran × Bld)^2 and ff	5 ♀ 6 ♂ low d among 68 ♀ 105 ♂ F_2	In later generations high-grade d is found; see text
2	Bd (Beaded)	F_1 bb^1/ClB × poi achi	3 ♀ among 80	Is Bd allele
3	ro op and bran^{dp}	F_2 (svr^{poi} × svr$^{poi\,h}$)^2	Few ♀ ♂ among many (1/8)	
4	bran^{dp}	F_1 svr^{poi} × svr$^{poi\,h}$	1 ♀ among many	
5	bran^{dp}, Bx	Stock 5145 poi dish	2 ♀ poi:dp, 1 ♂ Bx	
6	bran^r, Bx low allele	(Patt × 6317 achi)^2	1 ♂ Bx, bran^r segregates next generation	
7	b^B (dom. black)	F_1 px bl × bs	Few ♀	
8	dp (dumpy)	(px bl × X^9)^2	1 ♂	
9	bran, poi	(y × px bl)^3	1 ♂ soft bl among 309	px bl contained bs^{pp}
10	poi→+	(w poi × poi:dp)^2	1 ♂ among 52	
11	px	soft bl × (SD × soft bl)	1 ♂ among many	
12	vesiculated (vs) and l	ro op poi × +	½ ♂ missing, others vs	
13	N-Df	(ec br × ro op)^2	2 ♀ among 74	
14	L Lobe	(px bl × e wo tx) × e wo tx	26 ♀ 13 ♂ among 78 ♀ 88 ♂	New allele
15	L Lobe	(soft × poi)^2	5 ♀ 2 ♂ among 44 ♀ 30 ♂	
16	e allele	Stock soft bl 5085	1 ♀	Phenotype different from soft blist but genetically same
17	M	poi × Bld	A few	Sex-linked M sterile
18	e, L	(px bl × bw sp ba) × bw sp ba	2 ♀ e, 1 ♀ 1 ♂ L among only 8 ♀ 10 ♂	L sterile
19	dp–vo	(poi bl × X^9)^2 × px ec br	14 ♀ 4 ♂ among 95 ♀ 41 ♂	
20	d–dachs	(px bl × ec ct g)^3	3 ♀ among 82	Sterile
21	abn. abd	px bl × (px bl × bs)		Abnormal abdomen and male genitals, sterile
22	bran^1, giant, dwarf	bs × (px bl × Fla) and F_3		
23	bran^1, giant	(px bl × Ore)^3 and F_4		
24	bran^{dp}, dwarf	(poi × Px)^2		
25	M (3)	poi × Bld	1 ♂	See list of mutants
26	bran^{dp}, poi → +	(poi × bb)^6	1 ♀	
27	bran^{dp}	(poi × a px sp)^5	15 ♀ among 150 in 4 broods	
28	bran^{dp}	(poi × I(1)y$^{px\,bl}$ px/+)^2	1 ♀ among 79	
29	dp–vo	(poi:dp × bran)^2	1 ♀ among 64	
30	bran^r	poi:dp × bran	1 ♀ 3 ♂ among 110 ♀ 60 ♂	

In the foregoing tables a large number of apparent mutants were not included, because they defied analysis, though the type of their appearance strongly suggested "mutants," or in fact rarely surviving small duplications or deficiencies from small translocations. This interpretation is based upon the reappearance of some of these dubious mutants in many instances, their usual sterility, and also their appearance as a considerable number of individuals from crosses involving px bl and derivatives. The most frequent types are the dwarfs and yellowish dwarfs. Two hereditary types of dwarfs will be mentioned below; the others either were sterile or did not reproduce their type. To the same category belong types with short bristles or with missing posterior dorsocentrals, with rough eyes or small eyes, and with asymmetrical types of wings (1 wing strap-like, etc.) or eyes (1 eye small or missing) or antennae (- antenna without arista), etc. Innumerable such individuals were mated. The majority were sterile, which makes me believe that a genetic basis is to be assumed; the fertile ones did not reproduce their kind, which might mean that it was only a modification, but might also mean that a deficiency or duplication was almost unviable and only the normal segregants survived. Another phenotype of this category is abnormal abdomen. The occasional appearance of such individuals is a typical feature; they probably are not hereditary. But in a number of cases specific types of abnormal abdomen appeared in segregating broods, in up to one-fourth of the individuals, all of which had the same type: Once, all had defective not concresced tergites along the entire middle line of the abdomen; once, all abdominal segments alternated in all individuals; once, all abnormal females were without the last two abdominal segments (not retracted genitals but real loss of segments). In no case could the hereditary character be proved. But thinking of Blond translocation where the very characteristic (1)Df type may segregate in considerable numbers and again be completely absent in a series of simultaneous crosses, I am inclined to assume that in these cases also the segregating types are rarely surviving duplication deficiencies from small translocations which might be located only if by chance known loci were involved in the cross.

I am encouraged in this belief because once by chance such an occurrence was traced. A cross (no. 591) of px bl × yw produced 71 ♀ 58 ♂ + and one white female. Both this exceptional female and her brothers and sisters were checked and shown to contain neither a white deficiency nor a mutation to white in the px bl X chromosome (see p. 467). A test cross, bred from normal F_2 females with stock yw males showed some of these females to be normal, some heterozygous for + and yw, and one for w and +; further tests showed the latter to have been produced by crossing over between y and w. But in this cross an unusual array of abnormalities appeared with respect to eyes, wings, bristles, and size, as table 127 has shown. Most of these abnormal individuals were sterile. Whereas the X chromosome introduced originally from px bl turned out to be completely normal so far as the w locus was concerned, the exceptional white female must have been the product of changed dominance. In the following generations of test crosses the abnormal types nicked wings, small eye (also many abnormal abdomen, once 8 among 30 ♂), again appeared and were sterile. Part of the solution was found when white ♀ and ♂ extracted from no. 1032 in table 127 were crossed and backcrossed with X ple (9 recessive markers including yellow and apricot w^a). It turned out that in some of these crosses part of the segregating X^o males did not show any yellow; further,

that all crossover classes showed yellow, and all the reciprocal classes without yellow were missing. This indicates that from the original X chromosome the tip containing yellow, not white, had been broken off and translocated. The dominance effect of w found in the first instance was clearly a so-called position effect of the type of the cubitus interruptus effect, produced by a break near w. This was demonstrated in the w^a/w compounds produced in these crosses, which usually were more or less apricot but, in the presence of the translocation, white. Unfortunately, an enforced interruption prevented the salivary analysis, and the translocation was meanwhile lost (other details have already been reported, p. 467).

Among the many mutants at the svr and a loci there is one which in all cases of its origin seems to be connected with a definite rearrangement simultaneously present but not identical with the mutant. We have described above the type slender which is a combination product of $svr^{pol\ s}$ and the bran allele $bran^1$, the former producing soft wings (in addition to pale color), the latter having not much of a phenotypic effect if alone. The following is the story of the origin of slender.

A cross was made of a plexus blistered ♀ to a Florida ♂ (no. 665), with the intention of testing the crossover situation at the px and bs loci, and also the reciprocal cross (no. 668). F_1 was in accordance with expectation. Some F_1 flies were crossed to different second-chromosome stocks without unusual results. F_1 females were also backcrossed to bs males, likewise without unusual results. Two backcrosses of the bs females with reciprocal F_1 males (plexus blistered × Florida and Florida × plexus blistered) both gave unexpected results. It should be mentioned that the bs stock from Pasadena had bred true for generations and that numerous simultaneous crosses between the plexus blistered and the bs line had not yielded anything unexpected with the exception of one line, reported already, which had produced the dominant black-Deficiency (see table 148). These two backcrosses yielded:

1) No. 912 ♀ bs × (px bl × Flor). 38 ♀, 22 ♂ *all* giants.
Hatching of flies (at 25°) started only on the 19th day. The flies were extremely large and withstood ether for at least five times as long as normal flies. Their other characters (venation) were as expected in this cross. I mention that giants had once before been produced from dwarfs in the plexus blistered line, which makes a mutation in the Florida or bs stock improbable. The giant character was obviously dominant, though none of the parents were giants.

2) No. 913 bs × (Flor. × px bl). 39 ♀, 25 ♂ of the different expected types of venation, all giants as before. Breeding of giants from these broods resulted in the following F_2:

No. 1143 = 913^2
4 ♀ 3 ♂ giants partly short bristles, one with small eyes
57 ♀ 38 ♂ all grades from normal size to dwarfs (not classifiable)

No. 1146 = 912^2
20 ♀ .. ♂ giants
68 ♀ 21 ♂ intermediates
10 ♀ 10 ♂ dwarfs

No. 1147 ditto
5 ♀ .. ♂ giants
42 ♀ 44 ♂ more or less intermediate
4 ♀ 5 ♂ dwarfs

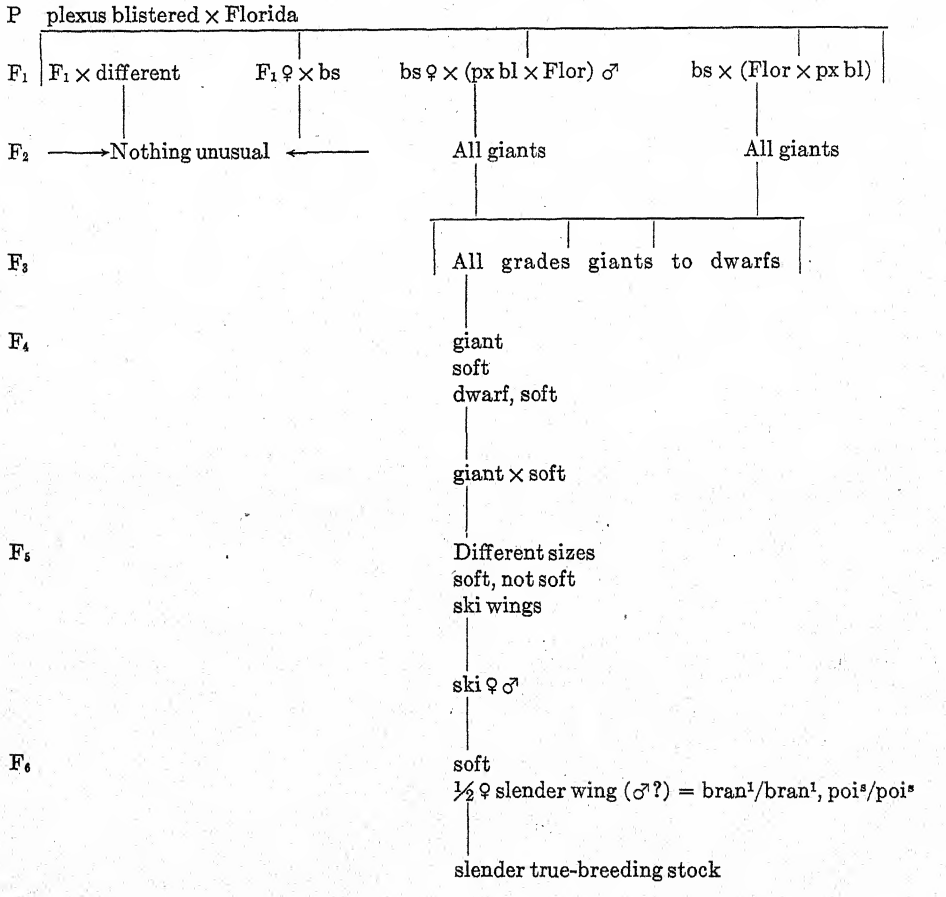
No. 1148 ditto
9 ♀ .. ♂ giants
80 ♀ 44 ♂ all grades intermediate to dwarf (not classifiable)

Most of the dwarfs had soft wings, i.e., the X chromosome from px bl with the mutant $svr^{pol\ s}$. The dwarfs and giants were tested in subsequent generations. A

giant line with a changing percentage of giants has been established, but a dwarf line could not be bred. One of the F_4 generations bred from intermediate-sized flies from 1147 (see above) contained 72 giant females (a few blistered) with normal venation, 12 males +, 18 males soft wings (males not giant); another similar one contained 25 ♀ giants, 2 ♀ with abnormal wings (unequal length, short), both being

TABLE 149

PEDIGREE OF slender = bran^1 + poi s



sterile, ♂ soft, 1 dwarf and soft. From the latter brood an F_5 was bred from the giant ♀♀ and soft ♂♂. It contained flies of different sizes, soft and not soft, and in addition (no. 1363) 2 ♀ 3 ♂ with ski wings. All these ski flies were mated and turned out to be rather infertile (see the low fertility in the foregoing generation). They produced altogether 30 individuals, females and males, part of the males with soft wings and half of the females with a new type of wing, narrow and slender, called slender (some of the males had the same wings, as tests showed, but hidden because of soft). From this brood (1410) one combination of slender females with soft wings produced all slender offspring, which since bred true (1436). Another brood gave

some slender offspring and a majority difficult to classify. The ski flies, then, had been heterozygous for bran^1, which obviously had arisen by mutation somehow connected with the giants and dwarfs in the presence of svr$^{poi\ s}$ derived from px bl. The pedigree table 149 shows the general features of the case.

On a later occasion the mutant bran^1 was again produced in connection with giants. In F_3 from px bl × Ore, giants were found, and also soft was present in the X derived from px bl. A giant ♀ with a soft ♂ (no. 2297) produced one-half normals (very large but not giants) and one-half ♀ and ♂ slender. No dwarfs were found, but it is possible that they were not viable and that actually only ¼ slender segregated. Slender bred true and turned out to be the bran^1/bran^1, poi s combination as before.

Once again slender was obtained (see pedigree, p. 367) in a way which required a mutation from poi bl to poi s and in adidtion from bran to bran^1. In this case both parents were dwarfs but no giants had been recorded.

Once, the opposite relation was observed. Among a great many outcrosses involving slender there was one, (slender × bw e ey)^2 no. 2053, in which a large number of giants segregated. Slender thus may still contain the ancestral condition which produces giants, or be able to reproduce it.

The interest thus centers upon the giants and dwarfs. Giants and dwarfs have repeatedly been found in *Drosophila*. Some of them behaved like ordinary mutants, but some offered difficulties to an analysis in addition to the variability of penetrance and expressivity (literature quoted in *DIS* 16). The most complicated case is that of Bridges's giant, which is stated to be based upon an unknown dominant, homozygous lethal in the second chromosome, in conjunction with a homozygous recessive near locus 64 in the third chromosome. The males, moreover, are sterile. But in none of these cases has a relation of giants to dwarfs been asserted. Such a relation, so far as I know, has been described only for the duplication deficiencies segregating from reciprocal translocations in Blond and pale, i.e., one of the combinations being giant while the opposite combination of duplication and deficiency is dwarfish. We expected, therefore, some such situation in our case. But neither translocation nor deficiency tests corroborated such an assumption and the salivaries seem to be normal, though one or two band alterations, difficult to find if the region is not known, cannot be excluded. The main facts found are the following:

1. From the pedigree reported above, a giant stock could be established. It breeds true, though the penetrance is very variable and real giants are rather rare in ordinary conditions, but increase, strangely enough, in old bottles. Male giants are rarer than female ones but are not sterile. Dwarfs are never segregated within this stock.

2. Apart from the cases mentioned, only once was a true-breeding giant isolated. It reverted to normal in the bottles after many generations. It seems that this was a different giant, identical with Bridges's giant 4 (2.24) as indicated by a localization test made before it reverted.

3. It is remarkable that giants (which could not be extracted) have also been obtained in the so-called achi lines, containing svr^{poi} and a high bb allele. Bridges-Gabritchevsky's giant also appeared in conjunction with a bb allele.

4. Dwarfs are the most frequent occurrences both in pure stocks of px bl and its derivatives and in all kinds of outcrosses.

5. These dwarfs have been tested innumerable times. They produced usually normal offspring in F_1–F_3.

6. Repeatedly, dwarfs appearing after the manner of mutants produced large, very large, or even giant offspring in F_1 and all transitions from giants or very large flies to real dwarfs in F_2. No true-breeding dwarfs could be extracted.

7. Only once (see pedigree of forked, p. 508) could dwarfs be isolated as a sex-linked mutant which had appeared together with forked and a bb allele. No giants were involved in this case.

8. When dwarfs segregated in F_2 out of dwarf grandparents and giant F_1, their numbers were extremely small.

9. While the extracted giant stock threw dwarfs, giants and dwarfs segregated in F_2 after outcrossing the stock.

10. These F_2 suggest a rather complicated situation which might be related to, though not identical, with Bridges's 2–3 giant. The following table (table 150) contains the results of F_2 giant × bw, e, ey)^2 only for the females. Out of 24 identical F_2, 4 contained only flies without size differences; the others segregated giants, intermediates, and dwarfs, with the exception of 3 broods without giants. The table contains the total numbers for all classes with the expectations for ordinary F_2 recombinations in all groups, as giants and dwarfs were present in all classes of the markers.

TABLE 150

(giant × bw, e, ey)^2♀ ♀

	Class							
	+	bw	e	ey	bw e	bw ey	e ey	bw e ey
Expectation for markers	27	9	9	9	3	3	3	1
giants : exp. markers	153	45	45	45	15	15	15	5
giants : number	171	29	69	16	11	14	6	4
intermed. : exp. markers	535	178	178	178	59	59	59	20
intermed. : numbers	638	204	210	59	49	21	32	7
dwarfs : exp. markers	81	27	27	27	9	9	9	3
dwarfs : numbers	67	53	24	5	23	7	6	4
Total : exp. markers	751	250	250	250	83	83	83	28
Total : number	921	286	303	80	83	42	46	15

The table shows in all groups the repeatedly discussed suppression of eyeless, which does not require further comment. There is no marker class without giants or dwarfs. But there is a clear reciprocal relation between the bw and e classes: among the giants there are 29 bw, 69 e, and among the dwarfs 53 bw, 24 e, the intermediates and the totals containing equal classes. This statistically significant difference can be interpreted as meaning that giants require the homozygous second chromosome from giant stock and dwarfs the third, the smaller number present in the two classes respectively being crossovers.

The ratios of giant : intermediate : dwarf in each class ought to be instructive. There is reason to believe that giants and intermediates cannot be clearly separated, though the error should be always of the same magnitude. But the counts of dwarfs are rather reliable. Looking at these ratios, we find the number of dwarfs much smaller than that of giants in all sufficiently large classes with the exception of bw and bw e; in bw there are 29 giants and 53 dwarfs, and in bw e 11 giants and 23 dwarfs as opposed to 17 : 67, 69 : 27, 16 : 5, 14 : 7 in the other classes. In the classes with many dwarfs the ratio not dwarf : dwarf is 293 : 76 = 3.9 : 1; in the other classes, 1198 : 106 = 11.3 : 1. This might mean that dwarf segregates as a simple recessive when the second chromosome from giant stock is absent, but in its presence is suppressed or lethal, maybe only in the homozygote.

The complicated situation indicated by these data is apparent also when the males are considered. In 9 F_2 broods in which the females behaved as reported, the males

did not show any size differences. In this case the sex ratio was 917 : 670 = 1.37 and significantly differed from 1 :1. In 10 broods the males were classifiable. In only two of them could giants be distinguished, which, however, may be due to poor expressivity. But dwarfs segregated clearly. In this group the sex ratio was 1018 : 924 = 1.1 : 1. The distribution of the dwarf males in the classes was:

Class	+	bw	e	ey	bw e	bw ey	e ey	bw e ey
Not dwarf : dwarf	434 : 47	111 : 47	93 : 31	33 : 7	22 : 17	8 : 5	31 : 5	19 : 7

This is a very different distribution from that found for females, the only clear high ratio being found in the absence of homozygous foreign chromosomes (the + class). No interpretation can be offered. But the sex ratios clearly indicate some participation of the X chromosome. Whereas the sex ratio is normal when dwarfs segregate, but one-fourth males are missing (sex ratio 4 : 3) when no dwarfs segregate, it is probable that in one combination of X chromosome and one autosome the males are lethal instead of dwarfs. Whereas the sex ratio is normal when the cross is made, so that all males have the X from giant stock, namely, (y, bw, e, ey × giant)$^{\delta}$, it follows that the foreign X (not from giant stock) is responsible for the lethal class.

It is remarkable that one of the rather frequent mutants, namely, bran^{dp}, recognized in the combination with poi called poi : dp (see p. 373), also seems to be connected somehow with dwarfism, as the following pedigree of one instance of its origin demonstrates. Test crosses for the analysis of the bs locus in poi were made. In two of them, nos. 5506 and 5507 (svr^{poi} × bs) × (svr^{poi} × Px^{1}) and (svr^{poi} × Px^{1})$^{\delta}$, one and two females of the wing type between pointed and dumpy, frequently occurring in the poi : dp combination, were found together with one male poi and dwarf (among 147 ♀ 146 ♂). The two not virginal mutant females were mated to their dwarf brother. Among about 150 daughters of different types (the mother had been prefertilized), 6 females of the maternal type and short bristles and one female with dumpy-like wings appeared. All had much plexation and therefore must have contained Px. A sister brood, also from not virginal mutant females, contained only one dumpy-like male, again with much plexation, and one male dwarf. Offspring of not mutant sisters were normal. Again the mutant females were not virginal when found and therefore were bred as mass culture. In the offspring, 3 ♀ 1 ♂ of the original mutant type appeared and 6 ♀ of the typical poi : dp features. From these a poi : dp line was extracted. The mutant bran^{dp} thus had appeared originally in a few gametes of both F_1 parents, while dwarfs were also produced. No more information about the coincidence is available.

Once more a similar relation was found, this time in connection with a return mutation in the a–px region of the second chromosome. We have described above (see p. 498) how in a px bl stock in which the y-Inv had originated the px mutant was lost by some reversion to normal. When these normals were extracted, their offspring contained (no. 3949) 4 ♀ 6 ♂ dwarf among 146 flies. Their offspring were very large though not giant. In a later generation dwarfs again segregated, but no rule could be established.

5. Summary of Mutants and Their Origin

In table 151 we have summarized the occurrence of mutation and return mutation at the px, bs, svr, and a loci as reported in the paper. This table contains by no

TABLE 151

FREQUENCY OF MUTANTS AT MAIN LOCI IN ALL RECORDED CASES

Mutant	In controlled crosses and checked				Found in mass culture of		Return mutation	Remarks	Σ In pair culture	Σ In mass culture
	From px bl	From svr alleles	From crosses within derivatives of px bl	From outcrosses	px bl	poi				
svr^{poi}	1	..	1	4	....	....	4, many times in bottle	Many times in outcrosses; not checked further	10	Many
svr$^{poi\,h}$	..	..	..	..	Many times	....	....	Only once from heat-treated Oregon	1	
svr$^{poi\,s}$	..	1 from poi	..	2	Many times	....	....	Most frequent mutant within px bl stock	3	Many
svr$^{poi\,sq}$	..	..	..	1	....	....	....	....	1	
svr$^{poi\,bl}$	1	1	2	..	Repeatedly	....	1 → poi	....	5	Repeatedly
svr$^{poi\,si}$	1	..	..	..	....	....	....	....	1	
svr$^{poi\,dish}$	..	..	1	1	....	....	....	Both cases in presence of poi and bb	2	
bran	1	1	2	1, many more	....	Many times	....	....	5	Many
bran^{1}	..	..	..	5	....	....	....	....	5	
bran^{2}	..	..	..	1	....	....	....	....	1	
bran^{3}	2	..	1	..	....	....	....	....	3	
bran^{4}	1	..	1	..	....	....	....	....	2	
bran^{db}	..	1	..	..	....	....	....	....	1	
bran^{dp}	..	2	1, 1 from bran	5	....	....	1	Many times more in all groups; most frequent mutant	10	A great many times
bran^{r}	..	..	1	2	....	....	....	Frequently from bran^{dp}	3	Frequently
Bran	..	..	..	2, from bran	....	....	....	....	2	
bs^{p}	..	..	..	..	....	....	2 and in bottles repeatedly	....	2	Repeatedly
bs^{pp}	1	..	1	..	....	....	Repeatedly in bottle	Repeatedly in stock	2	Repeatedly
px	..	..	1	1	....	Repeatedly	5 and repeatedly in bottles	....	7	Repeatedly

means all instances, but, in the main columns, only those in which the new mutants or the reversions have been extracted and tested. It is certain that some of them have occurred much more frequently (see last column), especially poi, poi s, and the poi:dp combination. Single individuals of the last-named (the combination resembling the case of "mutable genes") have been found so frequently whenever poi was present in crosses that they were not checked any more for their identity,

TABLE 152

SIMULTANEOUS MUTATION OBSERVED WITHIN ONE OR A FEW GENERATIONS INVOLVING SVR AND bran LOCI

(Details in text)

No.	Simultaneous (or almost) mutants	Origin from	Remarks
1	svr^{poi}, $svr^{poi\,si}$, $svr^{poi\,bl}$, bran, r; return high px → low, bs → +, px → +	px bl	
2	svr^{poi}, bb	Cross	
3	svr^{poi}, suppr. bs ba	Cross	
4	bran, poi → +	poi (many times)	
5	bran, $svr^{poi\,bl}$	poi × poi h	
6	$bran^{2}$, poi^{sq}	poi blist × Bld	
7	$bran^{1}$, poi s, giant	px bl × +	
8	Bran, $bran^{dp}$, $bran^{r}$, N	Bld × poi blist	
9	$bran^{dp}$, Bx	poi bb	
10	bran, $bran^{3}$, $bran^{4}$, poi, poi bl., poi si, poi dish, bb, px → +, bs^{pp} → +	px bl with bs^{pp}	
11	poi^{dish} from poi in presence of a, bb, bs^{pp}	poi × a px sp	
12	poi bl, bran, bs^{pp}, + → px, poi → +	poi × poi h	
13	bs^{pp} via notched	px bl	
14	bran, poi, px → +	px bl I	
15	e, $bran^{b}$, poi → +	soft blist	Not analyzed further
16	poi s, bran	poi	
17	poi s, bran	px bl	
18	poi bl, bran, px → +, + → px, spread	$I(1)y^{px\,bl}$ × px bl	Not analyzed further
19	$bran^{1}$, poi s, giant, dwarf	px bl × +, twice. Once giant from slender.	

which in view of the characteristic phenotype is, however, not doubted. The transition from poi to poi s is probably just as frequent, but cannot be discovered easily if not combined with bran, and even then it may be overlooked without tests because the phenotype overlaps with selected extreme poi. Further, bran has mutated much more frequently than is shown in the table. In the presence of px it might be overlooked, and since the combination px bran is poorly viable and rather sterile, it was not always isolated. Later on, occasional px individuals resembling bran were not tested any more. Thus the contents of table 151 may be regarded as only a minimum.

At many points of the foregoing discussion we could have drawn attention to the fact that mutants appeared simultaneously or what appeared to be simultaneously. As such cases are of special importance, they are tabluated in table 152. This table shows how frequently bran and poi alleles appeared simultaneously by mutation,

though they also were found to mutate alone. Further to be noted are the correlation between mutation at these loci and return mutation at px and bs, and the occasional accumulation of mutation to different alleles, simultaneous mutation at other loci, and special coincidences such as dwarfs and giants in relation to the "slender" combination.

LIST OF MUTANTS

Abnormal abdomen. A series of different hereditary types, none inherited in simple fashion or further analyzed.

b^B *Black dominant* from cross plexus blistered × bs. b^B/b is darker than b^B/+ or e. Small deficiency. See text figure 4. This Df(21)35CD puts black farther to the right than in Bridges's map.

Bd^G. Allele of *Beaded* (3–93.8). Origin from cross bb^1/C1B × 6340 achi (= combination of svr^{poi}, a px sp, bb^{poi}, and Y chromosome with bb). A slightly higher allele than the original Bd, with the same characteristics (incomplete dominance, enhanced to full effect by Inversions in third chromosome, homozygous lethal).

Bx^{G1}. Allele of *Beadex* (1–59.4). Origin 1 ♂ in offspring of pairs $svr^{poi\ dish}$ with bb (5145) together with $bran^{dp}$. Higher allele than standard Bx; otherwise same characteristics.

Bx^{G2}. The same, but lower allele from F_2 y bw, e, ey × 6317 = poi, $bb^{poi\ h1}$, and Y chromosome with $bb^{poi\ h1}$.

Bx^{G3}. The same not mentioned in text. Originated, after the tables were finished, from cross $bran^3$, $svr^{poi\ s1}$ × Df(2)a px, as 2 males.

Bxd. *Beadexoid* (1–±45). Origin 1 ♂ in F_4 from $bran^6$, $svr^{poi\ b1}$ × Bld which was simultaneously dachs of earlier origin. Phenotype like a high-grade Beadex.

bb^{poi}. Low *bobbed* from pointed (1–66.0). Phenotype described in table 75. Origin repeatedly in first chromosome from svr^{poi} and other alleles (see special section on bb). A similar allele also found in plexus blistered stock.

$bb^{poi\ h1}$. The same, but higher ellele; see table 75.

$bb^{a\ px\ sp}$. The same, but low allele in a px sp stock, brought out only after crossing to svr^{poi}.

$bb^{a\ px\ sp\ h1}$. The same, high allele. See table 75 and section on bb.

bs^p. *blistered*^{p} (2–107.3). A slightly higher allele than bs present in px bl stock. See table of phenotypes 79.

bs^{pp}. The same, higher allele present in px bl stock and repeatedly produced by mutation. For origin see special section; for phenotype and compounds see table 79. Frequently associated with small deficiency right of ba.

bran. *broad angular* (2–at or near arc). Probably arc allele (see special section). Originated many times from plexus blistered, svr^{poi} (see table 152). Wings broader, shorter, and blunt or broad at tip. At time of origin tendency to short bristles, later disappeared.

bran alleles $bran^1$, $bran^2$, $bran^3$, $bran^4$, $bran^{db}$, $bran^{dp}$, $bran^r$, $bran^X$ (from X rays), Bran. Some phenotype like bran, some normal with effect visible only in presence of svr alleles. For origin see tables 151, 152. For phenotype and combination effect see table 74.

curl. *curl* (2–±60). Originated in stock y × r from plexus blistered. Like low-grade Curly; characteristic combination effects with rudimentary.

d. *dachs* (2–31.0). At least four different alleles, a low one with little expressivity, one like standard d, an extreme one, and a dominant one; the higher ones completely sterile. Repeated mutants after crossing. See table 148. Also originated in $In(1)y^{px\ bl}$ stock in at least two alleles.

Df(1)ec. *Echinus deficiency* in stock plexus blistered. Minute characters. Completely sterile females, homo- (hemi-)zygous lethal.

dp. *dumpy* (2–13.0). Repeated, different alleles, lower like standard dumpy, higher with strong vortices. For origin see table 148.

dwarf. Most frequent type, segregating into and from giants; only one could be isolated as sex-linked recessive. All others seem rare surviving Df-Dp from small translocations, though not proved. See special discussion, p. 513.

e. *ebony* (3.70.7). Different alleles of a phenotype such as e^s, and higher. For origin see table 148.

enhancer of ebony (3–?). Once in a line of $bran^{dp}$, svr^{poi}. See table 148. Makes e^s/+ darker than e^s, and e^s/e^s darker than same with speck.

f^G. A *forked* allele (1–56.7). Not completely like standard forked; tendency to loss of posterior scutellars; sometimes individuals of a stubble type. Origin as three males from bran, $svr^{poi\ bl} \times$ (bran, $svr^{poi\ bl}$), the latter containing a second-chromosome homozygous lethal Minute. Poor fertility.

Giants. Different occurrences, never simple mutants, usually related to dwarfs and probably segregating Df-Dp from translocations. See special discussion, p. 513.

L^{G1}. *Lobe* (2.72.0). Origin (plexus blistered × e wo tx) × e wo tx. Different from other alleles by variety of effects. All the usual types and, in addition, a tendency to increase eye into a short finger-like structure or to split off small parts of eye and dislocate over head. Frequently short palpi inside modified eye. Dominance not very considerable.

L^{G2}. *Lobe* from $svr^{poi\ s} \times svr^{poi}$. Very similar to foregoing, if not identical with it.

L^{G3}. *Lobe* from (plexus blistered × bw sp ba) × bw sp ba. Like typical Lobe. Sterile.

M. *Minute.* Four different ones, one sex-linked, the others autosomal; not isolated or sterile.

Modifier of dominance of bran. Described in text; not isolated.

Modifier of viability of triplo-X. Makes triplo-X partly or completely viable; derived repeatedly from soft blistered but not isolated since the super-females are completely sterile; is autosomal.

$In(1)y^{px\ bl}$. *Inversion yellow px bl,* spontaneous as one male in px bl stock. See picture of salivaries, text figure 3.

op a. *Opaque arched.* Second chromosome recessive from cross $bran^{dp}$, $sv^{poi} \times$ bw e ey. Reverted to normal soon after establishment of stock. Wings opaque, cloudy, and arched.

rop. *Rough opaque.* (2d chromosome, probably different loci). Originated from cross $svr^{poi} \times svr^{poi\ h}$. Small minute like but usually normal bristles. Short rounded wings. Rough eyes or not. Δ formation at both attachments of posterior cross vein, tendency to doubling or tripling of anterior crossvein. Though true-breeding, difficult to recover after outcrossing.

Snipped-like. Rather exactly like $Df(2)vg^s$. 1 ♀ from $bran^6$, $svr^{poi\ bl} \times$ Bld. See table 148. Sterile.

Scalloped-like. A low nicking of the wings with very little penetrance; discarded.

sple. *spiny legs* (2–± 55). Derived repeatedly from $In(1)y^{px\ bl}$ stock and outcrosses, as described in text. At least 3 alleles. Lowest type, tarsal hair of forelegs like spines or thorns and irregular; medium type, all legs of this type; highest types, all legs of this type and disheveled hair on body. It is possibly identical with ti tarsae (*sic!*) irregular of Ives; see *DIS* 16.

su-poi. Suppressor for pointed. Found in cross $svr^{poi} \times bran^2$, $svr^{poi\ sq}$, autosomal, not isolated.

sv^{de}. Shaven depillate (4) from $bran^1$, $svr^{poi\ s} \times svr^{poi}$. Exactly like the description of this mutant, but completely sterile. Segregated in Mendelian ratios.

svr^{poi}. *pointed* svr allele and the alleles $svr^{poi\ h}$, $svr^{poi\ s}$, $svr^{poi\ sq}$, $svr^{poi\ bl}$, $svr^{poi\ sl}$, $svr^{poi\ dish}$, as described in table 74.

w. *white.* White eyes obtained three times, checked for allelism to w and discarded. One white from X-raying is small inversion of sections 3CD.

wD. *Dominance enhancer for white.* See analysis, p. 468.

y^{cu}. *yellow curled.* Pale yellow and slightly curled wings; from $bran^1$, $svr^{poi\ s} \times bran^2$, $svr^{poi\ sq}$. Sterile.

y^t *yellow.* Males as described with origin of forked; very light yellow. Completely sterile.

y^G *yellow.* Yellow allele from extracted giant stock, not mentioned in text.

IV. TENTATIVE X-RAY EXPERIMENTS

Although this work deals with spontaneous mutation, a few strictly preliminary X-ray experiments were made. The intention was to see whether the mutation rate under radiation would be unusually high in the px bl stock and whether the typical bran and poi mutants would appear. For these experiments the stock $In(1)y^{px\ bl}$ was used, i.e., px bl in which the small yellow Inversion described above had originated (thus marking the first chromosome) and which had also been used for experiments in spontaneous mutation (see p. 498). Those experiments served as controls. The stock was first inbred in brother-sister cultures and simultaneously checked for variability. Only once in 180 bottles was a sex-linked lethal present in the mother. The degree of plexation and blistering fluctuated in the usual way. Occa-

sionally a few dwarfs appeared. Males were irradiated with about 4,500 r, 9½ cm. from tube. The irradiated males were mated to either y or Canton females.[15]

In a first small series only 10 irradiated males produced offspring. Out of 16 F_2, 15 were normal, 1 contained 15 males among 117 with wings similar to bran and part blistered, both in y and not y classes. The type was inbred and tests showed that a new bran allele had arisen with definite features alone and in combination with poi, which are described in table 153.

Bran^x is thus more or less dominant. It resembles in many respects our bran^2 and bran^{db}. It is of interest that the yellow Inversion enhances the amount of blistering (best demonstrated in the cross y × bran^x, y-Inv). This is the same position effect of the right break of the yellow-Inversion already described (p. 399). (The presence of a poi allele was excluded.) Bran^x was never obtained in homozygous

TABLE 153

PHENOTYPES OF X-RAY-PRODUCED bran^x

2d chromosome	1st chromosome	Phenotype
bran^x.....	+.....	Between bran and +, varying up to real bran (i.e., ± dominant). Tendency to blisters
bran^x/+.....	y-Inv.....	The presence of y-Inv increases tendency to blisters (most individuals are blist)
bran^x/bran^x....	+.....	Never obtained, probably because bran^x is linked with px and lethal
bran^x/bran....	+.....	Wings dumpoid (between bran and dp)
bran^x/bran....	y-Inv.....	The same mostly blistered
bran^x/+.....	poi.....	All transitions from pointed blistered to soft blistered and folded wings
bran^x/bran....	poi.....	Rudimentary blistered

condition. It might be lethal *per se* as a kind of dominant. But bran^x had originated in a px-containing chromosome and was closely linked with this. Only one crossover px/px bran individual was obtained, but no bran without px. Since the bran px combinations are poorly viable and almost sterile, it is possible that this combination is responsible for the homozygous lethality and that, if separated, bran^x would be viable.

In view of a positive result with only 10 irradiated males, the experiment was repeated, and this time 25 fertile irradiated males were obtained. The results on mutation were very promising. Among four tests in crosses with y and involving only 18 X chromosomes, 1 w mutant was obtained which turned out to be a small inversion of sections 1, 3CD. (white had been obtained twice from px bl crosses, but in view of the frequency of this mutant this was not considered important and no salivaries had been studied). Further, among 20 crosses of irradiated males with Canton females, two different Notch deficiencies (in different crosses) and one Delta deficiency appeared among 520 females. Thirty-three of these females were bred to F_2, and four contained a sex-linked lethal. An additional feature was the unusual array of abnormal individuals in F_1 of Canton × irradiated ♂. We know, of course, that X radiation can produce phenocopies in the irradiated individuals.

[15] Mr. R. E. Paulson kindly performed these irradiations coincidentally with his own work. I am greatly indebted to the Department of Genetics of the University of California, especially Dr. E. R. Dempster, for the use of apparatus.

But here numerous abnormalities appeared in the offspring. Among 520 ♀ 465 ♂ the following abnormal types were registered (we are not repeating the dominant mutants already reported):

♀	♂
abnormal abdomen (1 contained a mutant)	2 blistered
1 gynandromorph	1 scute
1 abnormal abdomen and 1 wing bran	1 dwarf
1 short pointed wings	1 rough eye
1 one wing rudimentary; same side shorter abdomen, rough eye, 1 leg bent (not gynandromorph	1 strange wing shape
	1 low px (mutant)
1 one wing narrow, net, same side rough eye and shorter abdomen	1 one wing short
1 crippled	
1 short bristles (contains a mutant)	
2 one wing short (1 mutant)	

Only two of these turned out to be heterozygous for a new mutant, namely, one female with a short wing was heterozygous for a new bran allele and one male low px was heterozygous for bs^{pp}. Two more segregated mutants in later generations. Those with slight changes (scute, bobbed, abnormal abdomen) did not reproduce their character. The others were sterile. The frequent asymmetrical forms may be "mutants" with somatic segregation.

Further generations showed that more mutants had been produced. There was a bran allele, characterized by a little dominance and a tendency to blisters in the absence of poi, which was obtained in heterozygous condition in 4 males among 60, sons of the F_1 female with one wing shorter. This number is irrelevant because these 9 males were recognized by their dominance; other females and males probably were also heterozygous but not noticed. These males were crossed for testing to females with y and bran, and half of the offspring in both sexes were bran (part of the males blistered). The allele probably was $bran^2$, if not the ordinary bran. In one of three F_2 from this test cross a few dachs females and males segregated, and in a further generation of one of the F_2 which did not contain dachs, 6 dachs among 92 were obtained. Dachs thus had arisen somehow in connection with the new bran but was very poorly viable and almost completely sterile. We had earlier noted many instances in which different dachs alleles had been obtained from px bl crosses.

From the F_1 male with low px, i.e., more plexation than the ordinary dominance effect of px and bs (derived from the y px bl male), an F_2 with a sister was obtained in which the typical combination of px with the allele bs^{pp} (extreme px bl in both sexes) segregated. In a sister F_2 from normal parents 1 ♀ 1 ♂ of this type were obtained among a large number of the expected types. Thus bs^p had mutated to bs^{pp} in a number of gametes of the irradiated px bs^p males (tested with bs).

In one F_2 bottle from normal F_1 a few Minute-like individuals segregated. They were bred to bran and turned out not to contain bran. In F_2 the type segregated again but was subsequently lost.

We have already mentioned the one F_1 female with obnormal abdomen (6019). It produced with a normal brother only 2 ♀ and 5 ♂. Both females and one male showed a kind of pointed from which a new mutant type called slender-dumpy was derived by outcrossing to poi, the first male having been heterozygous for this character. This new poi allele has most remarkable features and is accompanied by a

second-chromosome condition. Details will be presented separately. In a sister F_2 from normal F_2, 1 ♀ 1 ♂ with broad and arched wings, probably a mutant, were obtained, both being sterile.

Finally, in the same F_1 (6032) which contained one Notch female a short bristled female was bred to a normal brother. In F_2, among many normal flies one female was found with yellowish color, rough eyes, and opaque wings. She was mated to a brother and in the second generation a new type segregated which turned out to be a low allele of broad (br) in the first chromosome.

Thus, among 520 females and 465 males heterozygous for one irradiated autosome (only the females for the X chromosome), of which only 30 were tested, in F_2, in addition to the 2N and one △ found in F_1, there were produced 4 sex-linked lethals, at least 1 bran allele, at least 2 instances of bs^{pp}, 1 dachs, 1 Minute (?), the new slender-dumpy = a poi allele, and 1 broad (br). Not only is this an unusually high rate of mutation, but the regions are involved which are known to mutate in our line, namely, bran, svr, facet-notch, dachs, bs. Thus the preliminary results are rather encouraging, and special experiments will be conducted as soon as feasible.

V. DISCUSSION

This paper presents data on spontaneous mutation and such facts concerning the genetic constitution of the mutating lines as could be found out. The general trend of these data is to suggest that mutation is not a haphazard event in a so-called gene molecule, but a phenomenon of a determinate, orderly type which is caused by conditions within the chromosomes. We prefer, at this time, to present primarily the factual data as they stand and not to enter into a full discussion of their bearing. We believe that such a discussion would be useful only if an attempt were made to analyze and correlate all the facts known about mutation and to confront them with our knowledge of the constitution of the hereditary material. We are confident that, even now, so exhaustive a discussion would cast serious doubt upon the reality of the so-called gene molecule; but in order to be convincing the discussion would have to be complete and elaborate, and not a short appendix to a factual paper. Hence, we propose only to mention such items from the foregoing analysis as, in our opinion, point away from the conception of chance happenings in a side chain of a gene molecule, and to indicate, not too specifically, in what direction a better solution for the problem of mutational changes within the chromosomes may be found.

The following groups of facts reported in this paper stand out as pointing toward the existence of certain rules governing the origin of spontaneous mutations.

In the main line and its descendants studied closely over a considerable time, definite loci show a tendency to mutate. This mutation produced repeatedly one and the same mutant, and frequently members of a allelic series of the same loci. Some of these alleles appeared frequently by mutation, others only once. The alleles include invisibles, recognizable only by combination effects; recessive and dominant alleles; one so-called unstable mutant (a second one was produced by X rays); and a few recognizable rearrangements. This applies to the arc and silver loci, both of which are otherwise normal in the salivaries, though remarkable features near by were described. Both of these allelic groups have a relatively high tendency to return mutation. The original stock contained mutants of px and bs. The latter

has also a tendency to mutate to a higher allele, and both rather frequently revert to normal. In normal descendants of reverted px, mutation to px can occur. In addition to these frequent mutants, other visible mutants are obtained from the original stock and its derivatives more frequently than usual after outcrossing. Most remarkable is the fact that, in rather small experiments with X radiation, mutation was produced at the same main loci (a and svr).

There is a remarkable tendency toward crowding of mutations. If, after crossing, a mutant appears, others will frequently be found in the same or subsequent generations. In a rather extreme way this is true for the mutants at the main loci. Reverse mutation of px and bs was repeatedly found simultaneously, though both loci mutated also independently. A very frequent occurrence was simultaneous mutation at the arc and silver loci, with respect to allelic mutants as well as reverse mutation. Again, mutation at these loci sometimes coincided with mutation at the px and bs loci, especially return mutation. Most probably there is also a correlation between mutations at the svr and bb loci.

In many cases, mutation was preceded by abnormalities which themselves were not inherited, e.g., scalloped wings, dwarfs, ski wings as parents of mutants which had nothing in common with these phenotypes.

The genetic analysis of the lines from which all these examples were taken revealed peculiarities which had to be interpreted as small nonreciprocal translocations and transpositions. Most of them involved the X chromosome and were therefore traceable through male lethal classes. Similar conditions in the autosomes not engendering known loci could hardly have been discovered. These abnormalities were present or absent in the individuals from nonselected populations, and, if present, some or all could be found. Only a part of them could be verified in the salivary chromosomes, involving only extremely small sections.

The salivary chromosomes of the lines studied showed a considerable array of small rearrangements, mostly of 1–3 bands, both deficiencies and translocations. Some of them were rather frequent, others rare, or very rare. Larger deficiencies, inversions, and translocations were very rare. This means the rearrangements above mentioned are present in the stocks without showing visible effects, and thus are in contrast to those rearrangements which have been connected with mutants. It is remarkable that a considerable number of these small rearrangements were identical not only in px bl, poi, and other alleles of the series derived directly or indirectly from px bl, but also in a completely independent mutant $svr^{poi\ h}$ without any genetic relation to the other lines. But different wild-type lines were free from these small rearrangements. With the lone exception of the ec locus, none of them seemed to include known loci and none of them were located at the loci of mutants appearing in those lines (except $bran^2$, which is a one-band deficiency). It is noteworthy that a considerable number of the small rearrangements are found in the neighborhood of the mutating loci, i.e., tip of X and right end of 2. But there is a suspicion that this is only evidence of closer scrutiny of the suspected regions. Finally, it ought to be said that, in two cases, mutation at the svr locus occurred in an X chromosome introduced into a cross from a tester stock, under exclusion of crossing over but in the presence of a bran allele. There is also one case in which, after X-raying sperm and crossing the X-rayed males, a mutant appeared in the nonirradiated chromosome at the svr locus. This requires an indirect causation of this mutant

by some unknown condition which had been produced in one of the irradiated chromosomes. The points mentioned before also suggest the probability of a causation of mutants at susceptible loci by conditions present or appearing at different loci. (See especially the coincident mutations and return mutations at the a, svr, px, bs, bb loci.) There are in the literature scattered observations of mutants which appeared some generations after X-raying or treatment with extreme temperatures.

Our own ideas in regard to the nature of mutation may be stated without detailed discussion in the form of the following working hypothesis. We start from the fact that the serial, polarized differentiation of the chromosome reveals the presence of a not very large number of sections (aside from heterochromatic sections) within which the different so-called point mutations are located and within which rearrangement breaks produce multiple alleles by the so-called poistion effects. The sections in question overlap under certain conditions (see discussion in Goldschmidt, 1944). The question has been frequently discussed (see literature quoted in former papers) whether it might be assumed that point mutations are small rearrangements. By definition a point mutation in *Drosophila* is assumed in the case of a mutant with normal salivary chromosomes in the decisive region and its immediate neighborhood. Thus we are confronted with the question, Is there a difference in principle between a mutant with a visible change in the chromosome and one without a visible change? As all other differences assumed to exist between both have broken down, we have to decide whether we shall dismiss the question because it is of no use to discuss what cannot be seen, or whether there are facts known which make such a discussion fruitful. I think that the latter is the case. Gottschevsky (1937) studied a Notch deficiency with clear genetic results, i.e., deficiency for the facet and split loci; but the salivaries were normal. He offered the interpretation that the genes must have been inactivated, an explanation which is really only a confession that the theory of the gene does not furnish an interpretation. Later, Demerec (1941) found other similar cases in the same region. But meanwhile it was discovered (Kodani, 1942; Goldschmidt and Kodani, 1942) that a single band in the chromosome is not a unit but a coil of chromonema with 4–6 perultimate chromomeres radiating from it. There is therefore no reason to doubt that within a single band deficiencies or inversions of some of these chromomeres are possible. Could these be the "point mutations"? Thus far, technical difficulties have prevented a final answer. But we accept such a view as a promising hypothesis since it brings all mutations into line as mechanical disturbances of the serial order of the material which constitutes the decisive part of the chromosome.

Such an interpretation, we believe, would place all the facts of mutation, including those presented here, on the basis of mechanical happenings within the chromosome as opposed to chemical changes within a gene molecule. (I realize that "mechanical" may also mean chemical in the end, viz., if a break occurs between units of a polymerized chain and these are united again in a different way, new bonds must be established; "mechanical" as I use it thus means a change at a supermolecular level involving only primary bonds, not side chains.) I am inclined to visualize the facts of mutation in the following way.

The general facts of mutation require happenings which might occur in the chromosomes of any cell of the cycle, i.e., in any nucleus in resting condition or at mitosis. Not much is known about the condition of chromosomes in the resting

nucleus of diploid cells, except ovocytes. The salivary gland and similar nuclei in the Diptera are the only clear examples. It is tacitly assumed that the completely synapsed condition of the resting chromosomes in these nuclei is a special feature of dipteran cells. I wonder whether this is not the typical condition of chromosomes in all resting nuclei? The behavior of the heterochromatin in resting nuclei, which seems to follow the pattern of behavior in the salivary-gland nuclei, may be cited in favor of such an assumption. This means that within the resting nucleus the condition of the chromosomes is such as to release the unknown attractive forces between homologues which produce the complete synapsis without chiasmata, as in the dipteran nuclei. In mitotic prophase this attraction ceases, maybe in conjunction with the growth of the split halves of each chromosome. (There are a number of data in older cytological literature describing tetrad-like structures in the prophase of ordinary mitosis.) Only in the Diptera is this attraction still visible in metaphase. The only other example known to me occurs in the division of cells of parthenogenetic frogs (see Goldschmidt, 1920). But in the latter case the homologues are the product of a secondary regulation in an originally haploid set, which might be a different situation. If the chromosomes are synapsed in the resting nucleus, the presence of a number of small translocations, etc., would produce the well-known abnormal synaptic configurations. These in turn would lead to stresses and torsions in the chromosome which might result in breakage, pulling out of small sections, reinsertion. If the chromosomes in the resting nucleus are completely stretched (including molecular unfolding), as might reasonably be supposed, the same breaks might occur within what corresponds to a salivary band. The result is the production of small invisible rearrangements and so-called point mutations.[16] I can visualize the possibility that the knowledge of the presence of small rearrangements at definite points of the chromosomes would permit a prediction of the sections in which new mutants are most likely to occur because of maximum stress. All the facts presented in this paper, as well as as many observations of other authors on some kind of controlled mutation, agree with an explanation of the type just presented, and at the same time create serious difficulties for the hypothesis that the gene molecule changes its side chains in mutation. Quantitative experiments intended to corroborate our viewpoint were started repeatedly, but each time had to be broken off, owing to unfortunate external circumstances, before they had reached sufficiently large numbers. We hope to finish them and to return afterward to a more detailed discussion of our conclusions, including a review of known facts which are in harmony with our viewpoint.

VI. SUMMARY

1. The work is based upon a stock and its derivations, namely, plexus blistered. Px bl is derived from standard px by mutations at the bs locus, together with the rise of different modifiers for plexation and blistering.

2. The starting point was a spontaneous set of simultaneous mutations in a controlled brood of known pedigree which included return mutation from px and bs to normal, and mutation at the arc, silver, and rudimentary loci.

[16] Though I am refraining here from a complete discussion of the literature, I might mention that recently Fano (Proc. Nat. Acad. Sci. Washington 29, 1943) pointed out that stresses along chromosomes and interchromosomal pulls influence the rejoining of broken ends.

3. A similar "upheaval" occurred twice again later in mass culture, producing the same return mutations and different alleles at the bs, svr, and a loci.

4. Mutation at the same loci, including the return mutations from bs and px to +, recurred repeatedly in controlled broods, some more, some less frequently.

5. This includes the mutation to a series of multiple alleles at the svr and a loci, and repeated mutation at the bs and bb loci; it includes also secondary return mutation from + to px, return mutations of the svr and a mutants to +.

6. Each of these steps was found to occur individually, but in a significantly high number of cases two or more mutations or return mutations (including mutation from one allele to another) occurred simultaneously, pointing to some interrelation.

7. In many cases abnormal sex ratios coincided with these occurrences. Detailed accounts relating to points 5–7 of a number of cases are given.

8. Though the mutation rate within px bl and its derivatives is very low, mutation occurs very frequently after crossing between these stocks, or after outcrossing. In this case, too, a tendency to an accumulation of mutants was observed., i.e., when one appeared, others were found, usually within a few generations, including alleles at the main loci already mentioned. Some of these (visible) mutants were found repeatedly and also in different alleles, e.g., Lobe, Notch, ebony, dachs. Some such cases are presented in detail, others are only tabulated. Though quantitative experiments could not be finished on a sufficiently large scale, the data are unequivocal.

9. Rather frequently, abnormal individuals were found which were sterile or which transmitted their character to only a small part of their offspring. In some cases these became the parents of completely different mutants.

10. There are many additional details in connection with the foregoing points, e.g., strange ratios of segregation, as well as sex ratios, and sublethality of homozygous bran when present together with px.

11. Many individual cases of simultaneous mutation suggest a relation of the type found in translocations with more or less viable deficiency-duplication classes with typical phenotypes, as in Bld or P.

12. In a small set of tentative X-ray experiments with this stock an unusually high percentage of mutants was obtained, and among them also the ones at the silver, arc, blistered, dachs, and Notch loci, known to mutate spontaneously.

13. The genetic analysis of px bl and the derived silver stocks revealed the presence of a number of special features present in addition to the already mentioned mutants at the px, bs, svr loci, X chromosome modifiers responsible for blistering in the presence of px and bs^p, other modifiers for the degree of plexation, and others for the expressivity of the pointed wing character of svr^{po1}.

14. The most typical of these features are nonreciprocal translocations of small sections, not containing known loci, from the X chromosome—near the left end—to the second near arc and to the third right of ebony, which are recognized by the presence of male deficient lethal classes. In addition, the data indicate a transposition of the same sections from the left end of the X chromosome, one to the right between v and wy, the other to near the right end.

15. These insertions were already present in the px bl stock—none, or one or more, or all of them simultaneously in different individuals—and are typical for the svr mutants. There seemed to be some relation between these conditions and the mutation at the svr and a loci.

16. It is remarkable that many of the same rearrangements can be present in an independent svr allele derived from Florida stock.

17. Some but not all of these rearrangements could be located in the salivary-gland chromosomes.

18. In the silver stocks as well as in px bl from which they originated the second and (or) third chromosomes contain suppressors for the expression of eyeless of different degree of action. In some alleles a dominance enhancer for eyeless was found with special features which were not completely understood.

19. The salivary chromosomes of px bl and its derivatives contain a large number of very small rearrangements, some of which are found in every individual, others being more or less rare. They were studied statistically. Larger inversions and translocations were extremely rare.

20. In the most frequent mutants, the svr alleles, the svr locus is always normal. But in a number of the alleles a typical disturbance is found 6 bands to the right. In one allele it is a 2-band inversion. In others the typical aspect had been interpreted as a 1-band inversion. In still others an interpretation of the minute disturbance was not possible.

21. At the arc locus only one of the mutants was a 1-band deficiency; all others had normal chromosomes. Among the other mutants were some visible deficiencies, but most of them had normal chromosomes.

22. Many other interesting features are found in the svr alleles, sometimes different in alleles of different origin, viz., dominance-enhancing actions on arc and ebony, suppressor action of bs and ba. The former actions have an autosomal basis, the latter are located in the X chromosome.

23. The different svr alleles have different phenotypic effects upon different characters, i.e., pointed wings, soft wings, suppression of speck and sable, and recombination effects with mutants at the arc locus. They are compared with the effects of other loci in the same region, namely, Blond translocation and the color suppressors. A discussion of all facts and their meaning for the understanding of small chromosome sections is presented.

24. The combination effects of mutants at the svr and a loci (including deficiencies) are studied. They are of interest for the understanding of epistasis and the phenogenetics of wing shape, which is discussed.

25. One of the svr alleles behaves like one of the so-called mutable genes. Its genetics is analyzed and interpreted without recourse to mutable genes. (Another such case involving the same locus has been produced by X rays and will be presented separately.)

26. Among the combination effects of arc and svr loci are those in which an inversion or translocation break in the svr region acts like an allele of svr. In one of these cases a small inversion is involved with the left break in the yellow region and a yellow position effect. Thus the effects at both breaks could be demonstrated. There is a discussion of this set of facts.

27. As the work was done with the px bl stock and its descendants, we tried to get as much information as possible about the genetic composition of this stock. The main data have already been summarized. The analysis required detailed study of phenotypes of compounds, which gave a number of results not directly connected with the main line of work, namely:

a. An analysis of wing plexation as produced by the second chromosome mutants px, bs and alleles, ba, net, Px, their compounds and combinations.

b. Data on special behavior of balloon and net, further on some new bs mutants.

c. Data on blistering as produced by the loci mentioned as well as by modifiers in the X chromosome.

d. Phenogenetic consideration of wing plexation.

e. An analysis of some relations between the actions of bobbed alleles derived from px bl homozygotes and the different action in compounds upon bristles and abdominal tergites.

28. A considerable number of incidental observations are scattered through the report, e.g., data on Bld translocation, on surviving of triplo-X, on blistering in a wild-type stock, on ec-Df in px bl, a Dubinin effect for the w locus, different dominance enhancing or suppressing combinations, and others.

29. A short discussion presents the author's conclusions on mutation as not entailing a chemical change in a gene molecule but mechanical disturbances of the serial order of the material which constitutes the decisive part of the chromosome, including those below the level of one salivary band.

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PLATES

PLATE 23

Wing plexation of a few different types in illustration of the description of phenotypes in table 79.

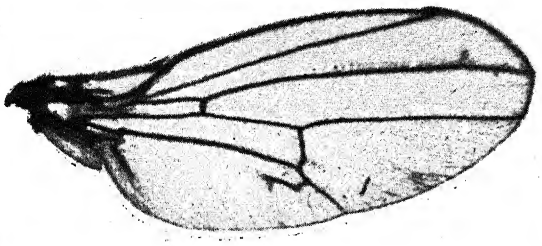
Fig. 1. The compound bs/bs^{p} with "antler" near posterior cross vein.

Fig. 2. The compound bs/bs^{pp} with "web" in the same location.

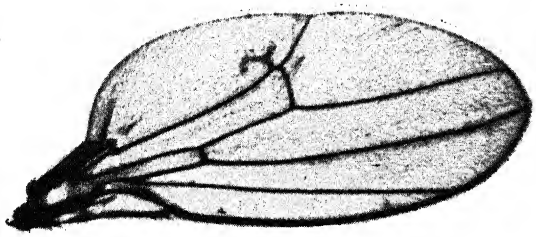
Fig. 3. Lower type of px bl with plexation in I and II, E.V. in V, antlers at 2, 3, 4, and web near cross vein. (The two wings are not completely symmetrical.)

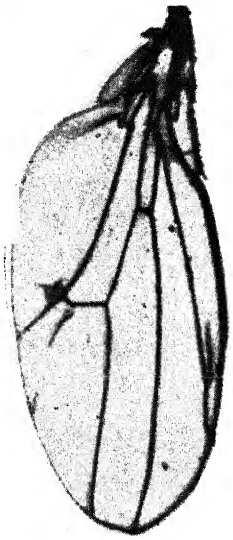
Fig. 4. Higher type of px bl, with complete parallel and periclinal veins (in right wings), antler or web at 2, 3, and large web connecting parallel and periclinal veins.

Fig. 5. Plexation of the mutant net with the large web at the posterior wing edge into which the ends of 4 and 5 merge.

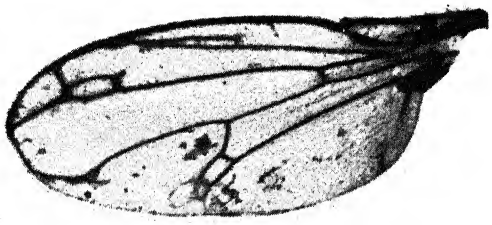


1



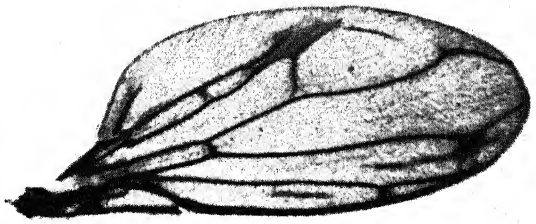


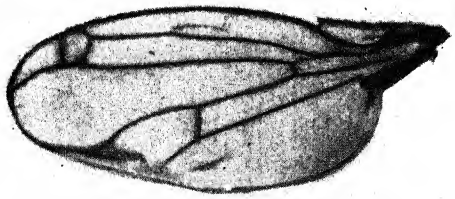
2



3

4





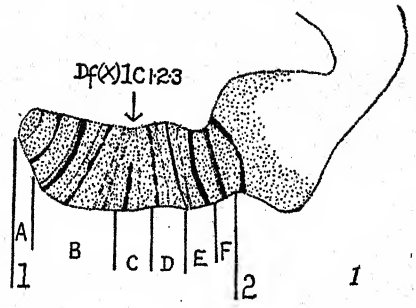
5

6

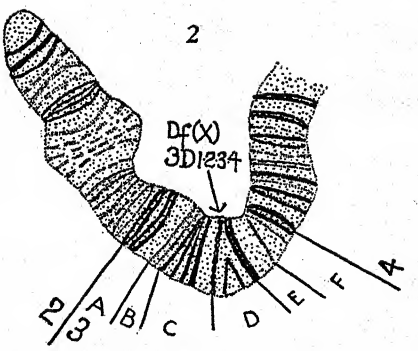
PLATE 24

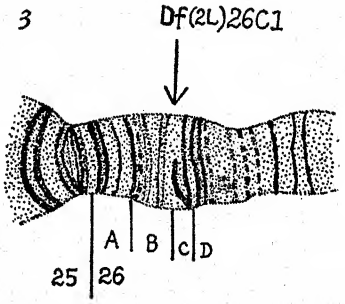
Salivary chromosomes in the test series of poi, poi h, and px bl as summarized in table 45, 46, 129. M. Kodani del.

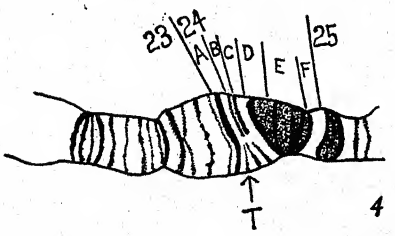
Fig. 1. Df(1)1C, 1–3 from px bl. See table 129, no. 2.
Fig. 2. Df(1)3D, 1–4 from px bl. See table 129, no. 5.
Fig. 3. Df(2L)26, C1 from px bl, not in main series.
Fig. 4. T(2L)24, AB from poi. See tables 46, no. 5; 45, no. 10; 129, no. 10.
Fig. 5. Df(2R)48D, 5 from poi h. See table 45, no. 6.
Fig. 6. Df(2R)53D, 8 from poi. See table 45, no. 7.
Fig. 7. Df(2R)58E from poi. See tables 46, no. 7; 129, no. 12.
Fig. 8. Df(2R)60D, 5, 6 from px bl. See tables 46, no. 8; 129, no. 13.

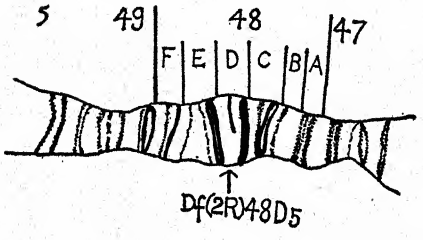

Df(X)1C1-2-3
A
B
C
D
E
F
1
2

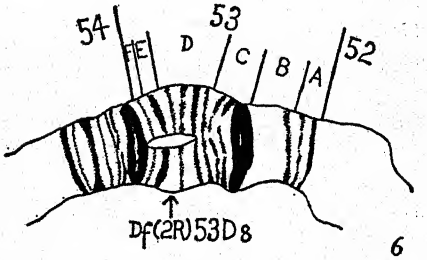
1

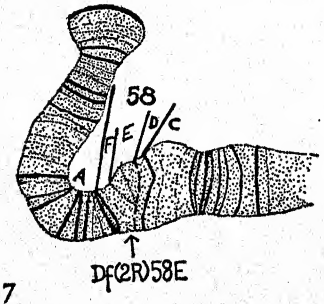

2
Df(X)
3D1-2-3-4
2
3
A
B
C
D
E
F
4


3
Df(2L)26C1
A
B
C
D
25
26


23
24
A
B
C
D
E
F
25
T
4


5
49
48
47
F
E
D
C
B
A
Df(2R)48D5


54
53
52
FE
D
C
B
A
Df(2R)53D8
6


58
F
E
D/C
A
Df(2R)58E
7

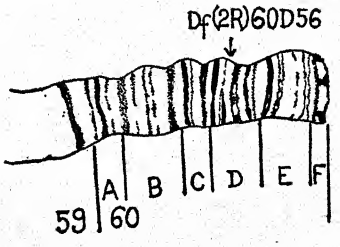
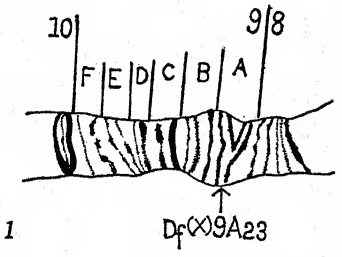

Df(2R)60D56
A
B
C
D
E
F
59
60
8

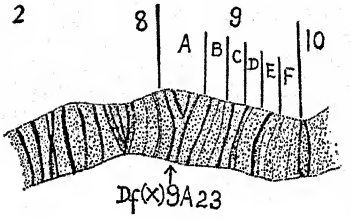
PLATE 25

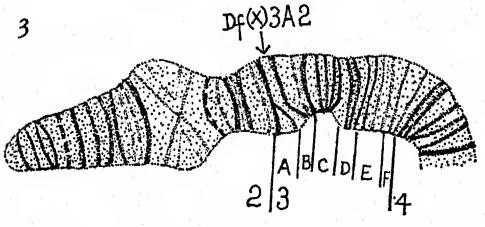
Salivary chromosomes in the test series of poi, poi h, and px bl as summarized in tables 45, 46, 129. M. Kodani del.

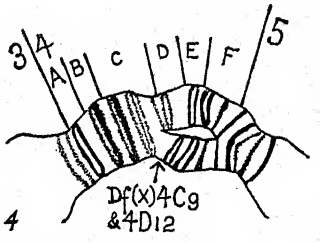
Fig. 1. Df(1)9A, 2, 3 from poi. See tables 46, no. 3; 45, no. 4; 129, no. 7.
Fig. 2. Df(1)9A, 2, 3 from poi. See tables 46, no. 3; 45, no. 4; 129, no. 7.
Fig. 3. Df(1)3A, 2 from px bl. See table 129, no. 2.
Fig. 4. Df(1)4C, 9 and 4D, 1, 2 from poi. See tables 45, no. 3; 129, no. 6.
Fig. 5. Df(1)4C, 9 and 4D, 1, 2 from poi. See tables 45, no. 3; 129, no. 6.
Fig. 6. Df(1)D5 from poi, not from series.
Fig. 7. T(1) right of 3C, 7 from poi. See tables 45, 46, no. 2.
Fig. 8. Df(1)9F, 13 from px bl. See table 129, no. 8.
Fig. 9. T between (1)12E, 8 and 9 from poi. See tables 46, no. 4; 45, no. 5.


10
9/8
F E D C B A
Df(X)9A23

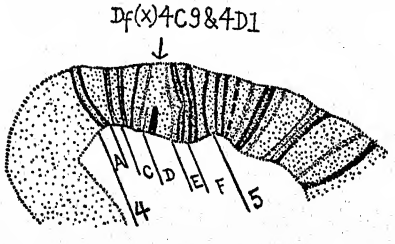
1

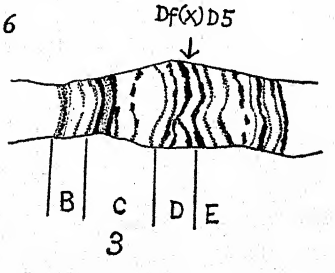

2
8
9
A B C D E F
10
Df(X)9A23

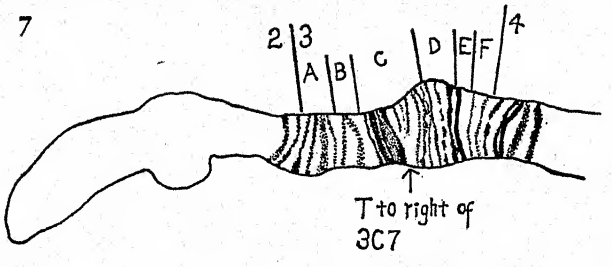

3
Df(X)3A2
A B C D E F
2 3
4

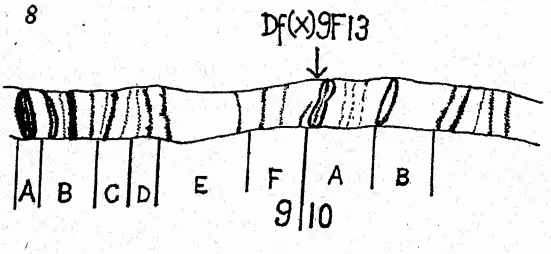

3 4
A B C D E F
5
Df(X)4C9
&4D12

4


5
Df(X)4C9&4D1
A C D E F
4
5


6
Df(X)D5
B C D E
3


7
2 3
A B C D E F
4
T to right of
3C7


8
Df(X)9F13
A B C D E F A B
9 10

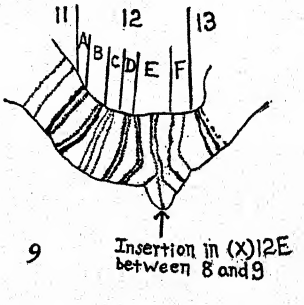

11 12 13
A B C D E F
9
Insertion in (X)12E
between 8 and 9

PLATE 26

Salivary chromosomes in the test series of poi, poi h, and px bl as summarized in tables 45, 46, 129. M. Kodani del.

Fig. 1. Df(2R)58D, 5 from px bl. See tables 46, no. 6; 45, no. 8; 129, no. 11.

Fig. 2. Df(3L)61C, 8 from poi. See tables 46, no. 11; 45, no. 12; 129, no. 16.

Fig. 3. Df(3R)91C, 4, 5 from poi. See tables 46, no. 15; 45, no. 16.

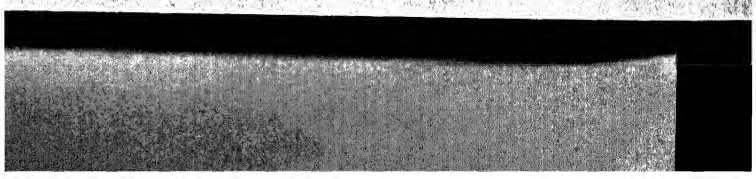
Fig. 4. Df(3R)84D, 6, 7 from poi. See tables 46, no. 13; 45, no. 14; 129, no. 19.

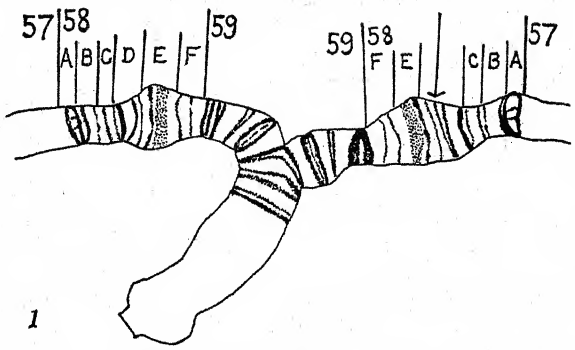
Fig. 5. Not from main series; Df(3R)86D, 1–E, ll translocated into 3L, 61, 62, shown in figure 8.

Fig. 6. Df(3R) 82E, 6 (7?) from homozygous poi; not main series.

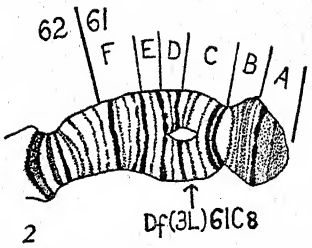
Fig. 7. Df(3R)86C, 6–8 from poi. See tables 46, no. 14; 45, no. 13; 129, no. 21.

Fig. 8. See figure 5.

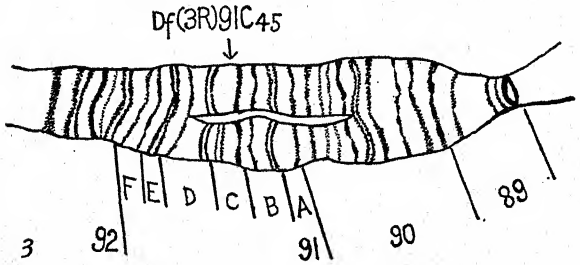



57 58 59 59 58 57
A B C D E F
F E C B A

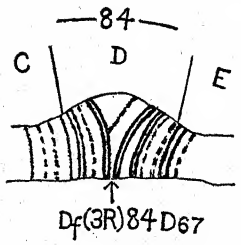
1


62 61
F E D C B A
Df(3L)61C8

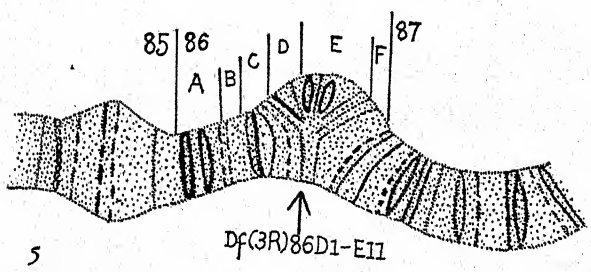
2


Df(3R)91C45
F E D C B A
92 91 90 89

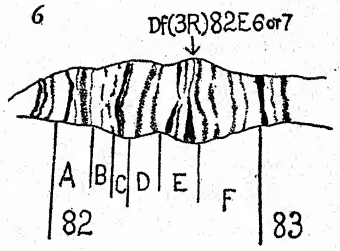
3


84
C D E
Df(3R)84D67

4


85 86 87
A B C D E F
Df(3R)86D1-E11

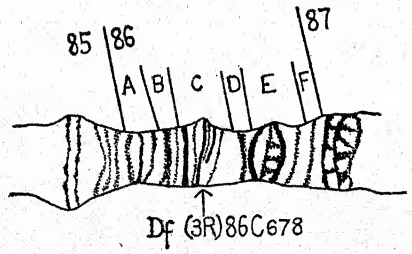
5


Df(3R)82E6or7
A B C D E F
82 83

6

7

8


85 86 87
A B C D E F
Df (3R)86C678

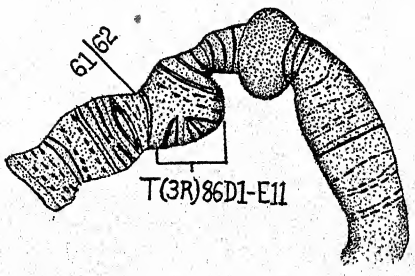
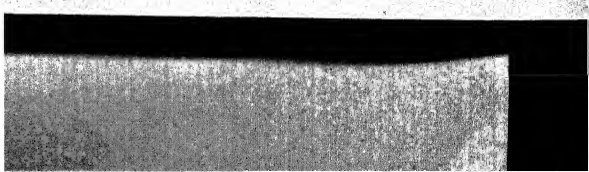
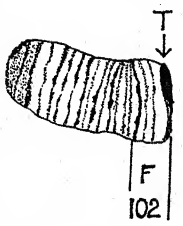

61 62
T(3R)86D1-E11

PLATE 27

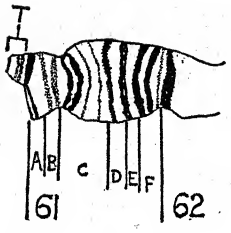
Salivary chromosomes in the test series of poi, poi h, and px bl as summarized in tables 45, 46, 129. M. Kodani del.

Fig. 1. T to tip of 4 from px bl. See table 129, no. 23.
Fig. 2. T to tip of III L, if not "pseudo translocation." From px bl.
Fig. 3. Df(3L)61C, 8 from px bl. See tables 129, no. 16; 46, no. 11; 45, no. 12.
Fig. 4. Df(2R)60F, 4–5, right of bs, ba, from px bl. See table 129, no. 14.
Fig. 5. I(?) near b–pr found in px bl, not main series.
Fig. 6. T(2L–3L) found in heterozygous rudimentary from px bl.

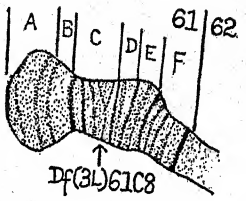



T
F
102

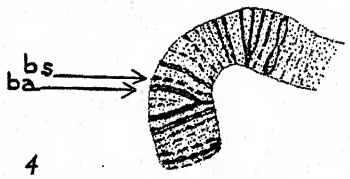
1


T
A
B
C
D
E
F
61
62

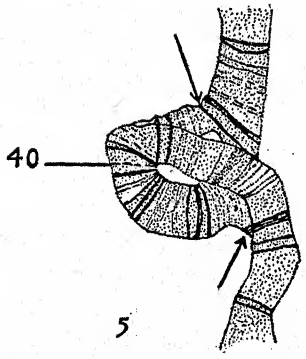
2


A
B
C
D
E
F
61
62
Df(3L)61C8

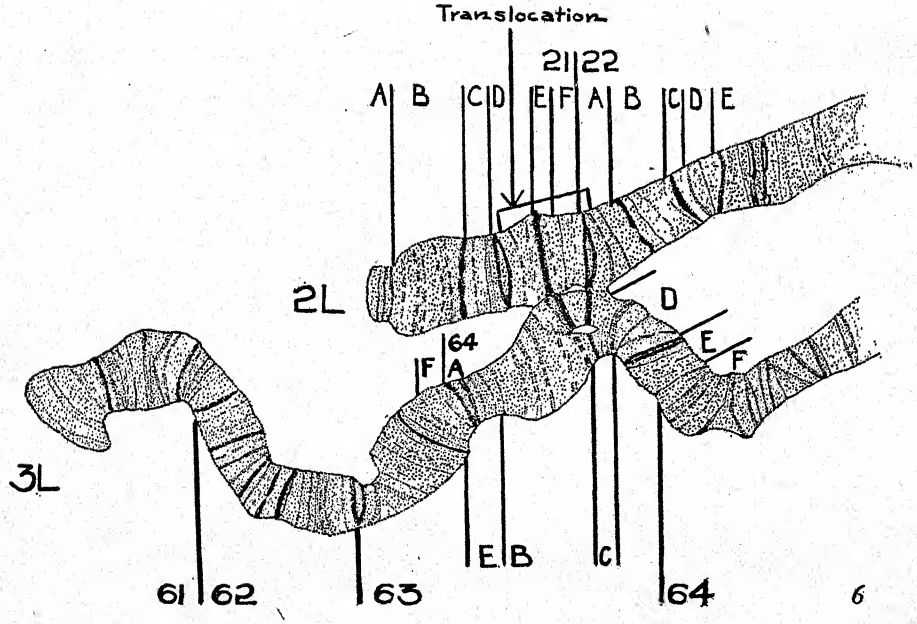
3


bs
ba

4


40

5

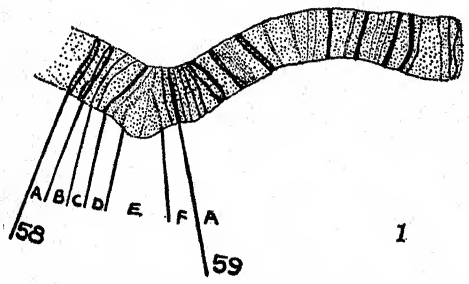

Translocation
21
22
A
B
C
D
E
F
A
B
C
D
E
2L
D
E
F
64
F
A
3L
E
B
C
61
62
63
64

6

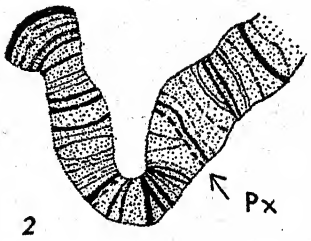
PLATE 28

Figs. 1–3, Kodani del.; others, Hannah del.

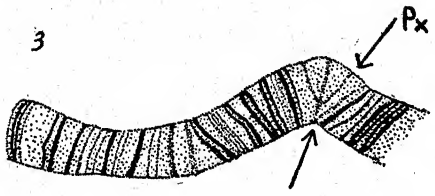
Fig. 1. Tip second chromosome px bl homozygous.
Figs. 2, 3, 4. Tip second chromosome px bl heterozygous.
Fig. 5. svr^{poi} insertion in 1, 3C9.
Fig. 6. svr^{poi} insertion 2R, 58D between 2 and 3.
Fig. 7. $svr^{poi\ s}$ Df1, 9A1–2.
Fig. 8. $svr^{poi\ h}$ insertion 3R91B.


A
B
C
D
E
F
A
58
59

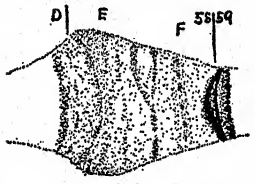
1


Px

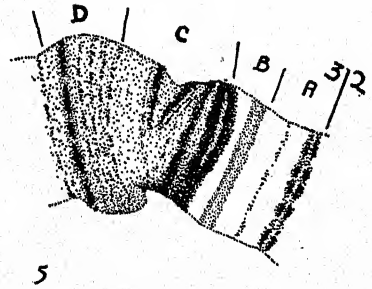
2


Px

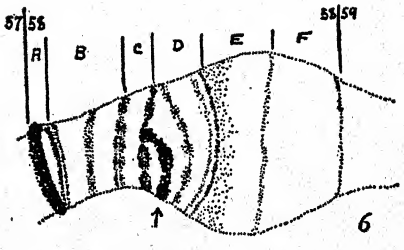
3


D
E
F
58
59

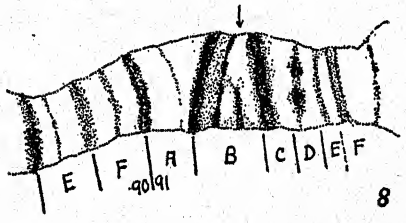
4


D
C
B
A
3
2

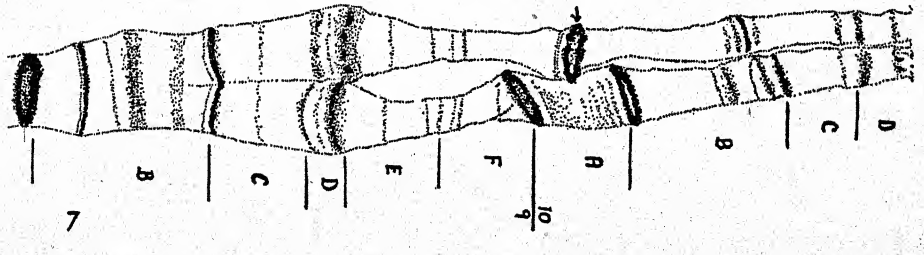
5


57
56
A
B
C
D
E
F
58
59

6


E
F
A
B
C
D
E
F
90
91

8


B
C
D
E
F
A
9
10
B
C
D

7

PLATE 29

Hannah del.

Fig. 1. The arc region of bran^{2} (combination bran blist). The 2 not synapsed chromosomes with Df2R, 58D6, 7.

Figs. 2, 3. Same region, synapsed; both heterozygous.

Fig. 4. svr^{poi}/+. The region 1, 1E1–4 showing at some foci an apparent crossing of 1, 2 with 3, 4, explained in text as a 1-band inversion (of 3, 4). Four different foci drawn.

Fig. 5. The same region in poi sq/+, two foci.

Fig. 6. The same region, poi/+, 3 foci.

Fig. 7. The same region, 2 foci.

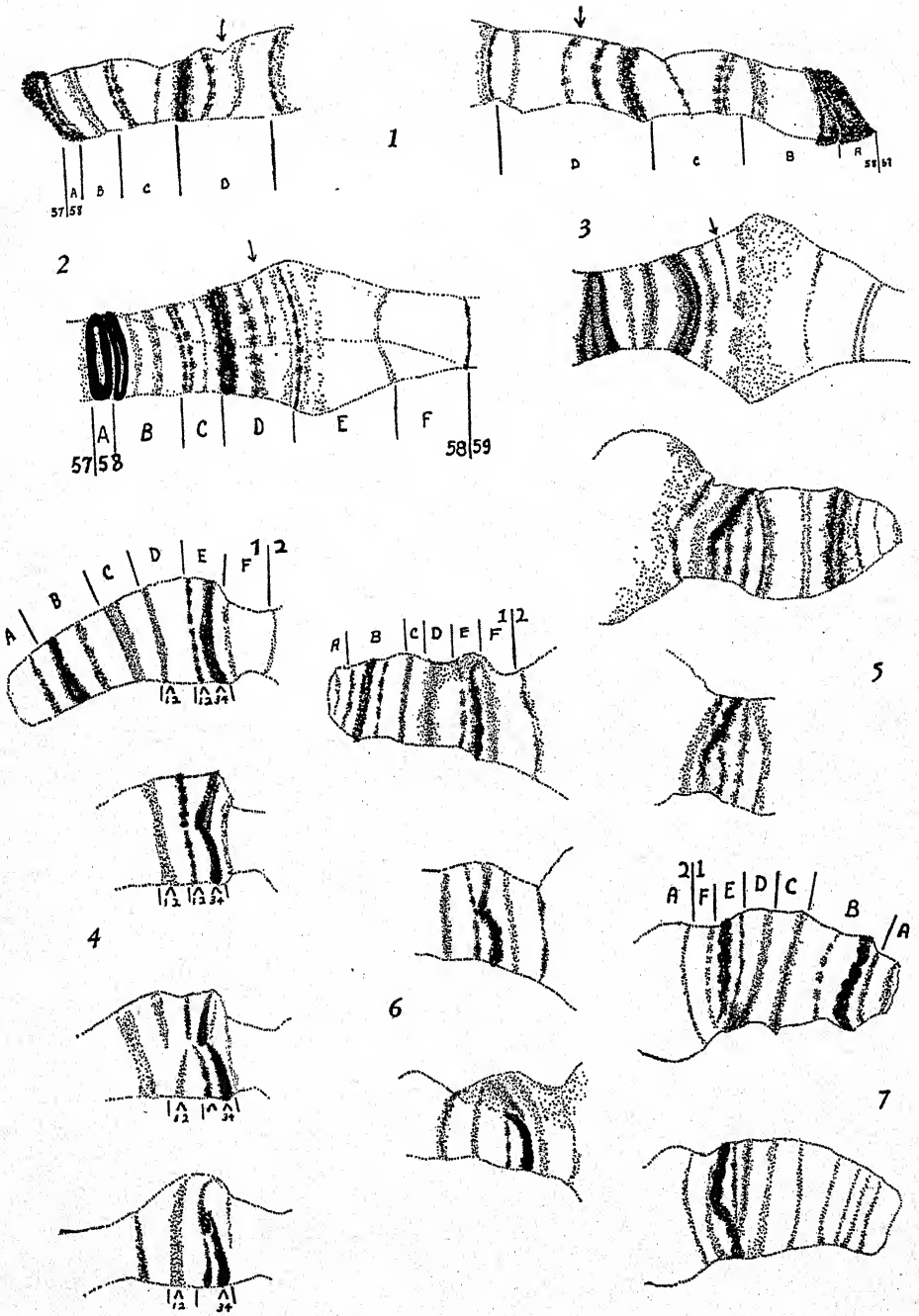
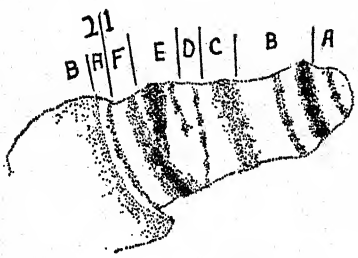

1
A
B
C
D
57|58
2
A
B
C
D
E
F
57|58
58|59
3
4
5
6
7
1
2

PLATE 30

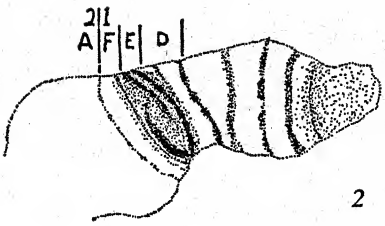
Hannah del.

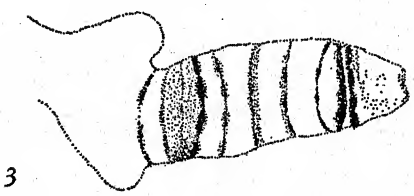
Figs. 1–4. Homozygous and heterozygous $svr^{poi\ h}$ with unanalyzable features in 1, 1E1–4.

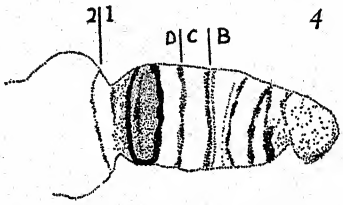
Fig. 1. Homozygous in 3 foci.
Figs. 2–4. Heterozygous.
Figs. 5, 6. Top of X of $svr^{poi\ s}$/+ drawn at 3 foci; inversion of E1, 2–3, 4.
Fig. 7. The same region, homozygous, reversed order E3, 4–1, 2.

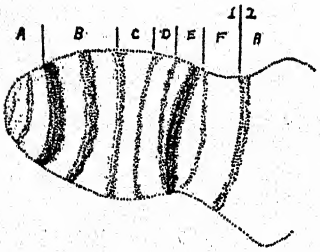

2 1
B A F E D C B A

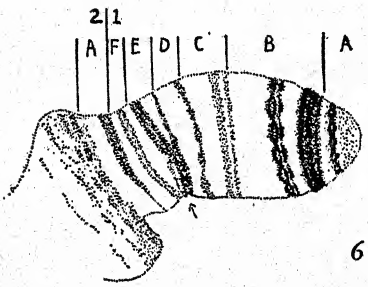

1


2 1
A F E D
2

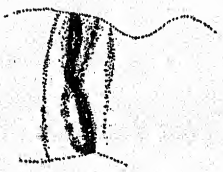

3

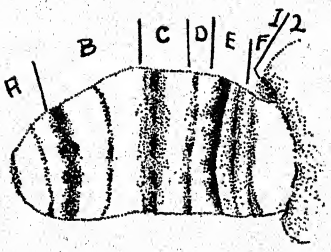

2 1
D C B
4


A B C D E F 1 2 B


2 1
A F E D C B A
6


5




B C D E F 1 2 B
7